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(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

15 A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

25 Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

25 The direct analysis of the sequence of polymorphisms of the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(\text{AA}) = x^2$
 Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$
 Single Heterozygote: $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
 Both Heterozygotes: $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(\text{ID})$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25
$$p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(\text{ID})$ and $p(\text{exc})$.

The cumulative probability of identity ($\text{cum } p(\text{ID})$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30
$$\text{cum } p(\text{ID}) = p(\text{ID1})p(\text{ID2})p(\text{ID3})\dots p(\text{IDn})$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- The probability of parentage exclusion (representing
- 30 the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a
5 Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next
10 generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),

20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, supra. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,
5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15

EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGCTCT GAAAACCTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTTTC/TJAGTTAATGCTGTCCTGTCAG
WI-7070	226	CT	---		---	AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT GATAATACATAAGCCCTAGGATTAGATACAATCTTGAAGAAACTGAGACAGATAATTCGAAAT AAATGAGGTAAAGTTTCAGGCACCTCA
WI-10744	61	GC	---		---	GGGCAAAATACCAGCAAAAAGTCAAAATACCAGCATCAAAGTCAGGTGCCAAAGGAGGTAGAACAA TTACAGTAACATATGTCAATCTTTTGTATATAGTATTTATCTGCCAATGCCGTAGATAIC/TJAGTG GGTCCCTAATAGTATTAGTTCTTTTCTCCTCTTCTCAATCTCTGAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATCTTACTGAA
WI-9975	126	CT	---		---	GCTAGGTTTGTGTTGGTGTCTTCACTAGACTGAGATGACTTGATTACAGTAATCCCTATGT GATGTAACCTAGCTAGACCTTCCCTCTCCGCAATCCAGCTCCAGTTTCAGAAAGTATGCCACAC TCAACCTTCTCTCCAGTTCACTCTGTATTAATTTCTTCCCATATTAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAGAGATCCCAAGTGGTGGG[G/T]CTT
WI-8010	247	GT	---		---	GCCCGGCTATCTTTAAATTTAACTTGATCTTTGGTGTCTCCATCCTAGGATCTGCCTATAAT CTTTGTCTGTCTGTA[G/C]ATTAACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCACAGAA
WI-5222b	85	GC	---		---	GCCCGGCTATCTTTAAATTTAACTTGATCTTTGGTGTCTTCCATCCTAGGATCTGCCTTAT AATCTTTGTCTGTCTGATGATACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCACAGAA
WI-5222	52	GC	---		---	TATGCACITCCACAAAAGCGATATAATTTAAAGTTTTTTTCAATAGAAATAATGTATAAAAATAA ATATGTTATTATAGGCATTTTACTAATACTATAGTCTCTTGGGAAGGAACACCCCAACCAATAGCTT ATAAAGTACATGTAAATTTATAGTAACATATTTACTATATACATATGGAATAATCATATTTCTCACA GAAGAGCTGAACAGACATTCACAGGATACGACTGTTGGAC[C/A]AGCTGCTG
WI-8007	242	CA	---		---	TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTCATGTATGTGTTTTGTTAG TCTATATTACACATATGAGTGAAATTT[C/T]GGGGCATGGGAAATACATCTTTATGAGACATTGA ACTGCTCACCACATATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTAC ATGCTTTCCAAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC
WI-9823	97	CT	---		---	

WI-9651b	105	A T ---	---	---	TCCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTTCCCT ACTTGCTCCTCATGTACAAATTTTCTGCTGCTCCTTCA/TJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCAGCTGCCAGGGACCCCTTATAGGCTCTG TCTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGTCCTC
WI-9651	139	T C ---	---	---	TCCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTTCCCT ACTTGCTCCTCATGTACAAATTTTCTGCTGCTCCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CT/CACAGGTACAGCCGACCATGCCCTACCTCCATGGCAGCTGCCAGGGACCCCTTATAGGCTCTGT CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGTCCTC
WI-7676b	309	A C ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTGCTGGGACTTGGCCCTGCTATTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCGGCTTCTTTGGTCTGCTGGGTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139	C T ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTGCTGGGACTTGGCCCTGCTATTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GC/TJGGCTTCTTTGGTCTGCTGGGTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105	G A ---	---	---	CATTATCTTGCTGGGCTGTTCAATTCATCTTCCCTCTCCTCCAAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGTGTGAATATTTTGTG/AJTGACTCCTATGCACATGATAAAATTTGTTA TGCTTGCTCTATCTATCTTTTGTATAGGAGTTTGGCCCATGACCCCTTTATGAGGAGAAAAGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	T C ---	---	---	TTGGTGTGAACCTCAGAATATAGGGAAAATAAGACAAATTTGAAT/A,CJGTACCCAGGAAACAAGAG CCCTGCACTTGACTCCAAAAGGAGTCTATTTCTGGCTGTTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACAATGTCA ATATCAATAGCATGCATATGGGTGTGGATTCTTAGMACTTATTGCAATT
WI-7041	174	C A ---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCTCCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTGCATGGCTCTATCCCTCTATCCCTCTGCTC/AJCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGAACAAGCTCATTGTACAGTGTCTGTATGTAATAA
WI-7224	134	T C ---	---	---	ATAAACCTTGTGTATGTATCACCCCAACTCACTAATATCAACTTATGTGCTATCAGATATCCTCTCT ACCCCTCACGTATTTTGAAGAAAATCCTTAACATCAAACTTATCATCCATAAAAATGTCAGCATTT /CJATTAANAACAATAAATCTTTTAAAGAAACATAGGACACATTTTCAAAATTAATAAAAATAAAG GCATTTAAGGATGGCCTGTGATTATCTTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	---	TCATTATGCAATTCACAGTAGCCCATGAAGTAGGTAAACCAGCCTCTATTTAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCCTAATAAGCAAAGACCTGCA/C JCCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCATGCTGTGCTGTCAGCCAGGACCCCATGGCA GAAAGCCCAAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	---	AGATCTGCCATTAGTATTTATCTTTGAAGATACCTTTGGAGATTCAITTTCTTGGTGGCACTGCAT GCTCATTGAGTGAACCTTTGTGGGTATAGAAATGGAATGGAGAGTTTCAACAGCTTTGCTGAAC TGACTTTGGG/GA/CTCCAGACTTCACCTGCTTGGCATTTGAACCATCACCTGGTTTGCAATCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T --	---	---	AAACACACAGAAATCATCAAGCAC/GA/CTGTGTTTGGAGATAAATGATGCTGAGTCACCTATG TAAGAAAGTAAGTCTGAAATAGTAGGATAGTATTAATTCCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTCAATCTATGGAACCTCCTGTAAGTAAATTTTCTATGGAACCTCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAATAAGAACACCTTTGAATGGCTTGTC TTTCAATAAAGAGAGTACATGATTGAACATGTGTTTAGATAAAGGGCACTT/GTGCAGGAGTGT TTAGGATGAAGAGAGAGAAATTAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 T G ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTGTTGGGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCAAGTACTTGAAGTGTGAGAGT/GTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCAIGTAATTGTATTCAATCAACAATTCGTCTGCTATGCTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCACTTGTCACACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTGTTGGGTGAGCGGATT AT/GA/CTGACGCCATGGGTGTTTCAAGTACTTGAAGTGTGAGAGTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCAIGTAATTGTATTCAATCAACAATTCGTCTGCTATGCTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCACTTGTCACACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	---	TCAACACGCTTTTATGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTACCCCTGAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCTCTGCTGAGAGGGAGGGCCAGACAGGGAGGAATTCAGGGGCATGTATGGCTC AGTCCCACTTCT/GA/CTGCAGAGTATAGGGACCAGGGTTCCAACTTT
WI-9484	178 G A ---	---	---	TCAACACGCTTTTATGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTACCCCTGAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCTCTGCTGAGAGGGAGGGCCAGACAGGGGAGGGGAGGGGATTCAGGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAACTTT

WI-7330	207 C T ---			AGGATGGAAGGAGACACGGGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAAATTTCTTTTAAATGTGGCATATAGGTTT GTGACACAAGAAAGTCATCTTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAAG TGAGAG[C/T]TGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACAG
WI-9443	211 G A ---			TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAGGGATGTATTACAAATTTAAATGAATCAGTCACCT GCACAAATTAATCTCTTGGCATACAAACTGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACACTCATGGAAGGCAGCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCCACATGCCCACTT
WI-7166	59 C T ---			TCTCTCAAAGAGAAAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCTTGTGCAAAATATTGACTATTCTGTATCTTTTCATCTTACTAAATTCGTG ATTTTCAAGCAGCATCTTCTGTTTAACTTGTGCTGTGAACAAATGTGAAAGAGCTCTTCCAAT TAATGCTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189 T C ---			GCTTCTCCCCAGGAAGGGGCTCTTGGCTTGAACCTTCCAGAGAGGGGGAGCAATTTTAGCC CCACCTGTCCCATCTGCCCTTCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGGGCT GCGAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAG[C/T]GGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTCAGGGGCCCACTTCCCTGGAGCTC
WI-7259	188 G T ---			GCTTCTCCCCAGGAAGGGGCTCTTGGCTTGAACCTTCCAGAGAGGGGGAGCAATTTTAGCC CCACCTGTCCCATCTGCCCTTCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGGGCT GCGAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAG[C/T]TGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTCAGGGGCCCACTTCCCTGGAGC
WI-7322	275 A G ---			GTACTTTAGGCTGTGGAGGTGGCAATTTAGTGTGACCTTGCACAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCATATG GCCATAAACTGCTAAGCACTCAGGCCCTCCCACTCATCAACCCCTTGACCAGAGAAAGAACCTC TGGTCTCTATCCCTTGTACATAGAGAGTTTGTGATGGGGCTCTTGCTG
WI-7685	46 T C ---			TCAGTTCTAGTCTCTCTGGGGCCACACAGAACTCTTTTGGGCTCT[C/T]TTTCTCCCTCTGGATCA AAGTAGGACGAGGACCATGGGACAGGCTTGGAGCTGAGCCTCTCACCTGACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCCTAGCCTTATCTCTGATCTCCATGGCTTCCCTCCCTCTGCCGACTC CTGGTTGAGCTGTTGCCTCAGTCCCCCAACAGATGCTTTCTGTCTC
WI-563	87 G A ---			TGTGACCAATTGTTATTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTGGCCAGAAATTC CTGGGGGAGGGCTCCCC[G/A]CCCTGATCATGTCTACCTAAGTGCCTACTCTAACAAATACTACTOC TGTGATATGGGATCCTAAGCCAAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGGCACAT

WI-931c	191	C A ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCTCT GTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-931b	81	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCT TCTGTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-931	31	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCAC[A/G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCT TCTGTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCTCCC
WI-10870	103	G A ---	---	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACCTACTTAG[A/G]CAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCTCCC
WI-7719b	281	T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATCTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCTCACIGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATCTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCTCTCACTGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTGGAGTATATCTAACTGTGGCCTCCACTTTCATTTTCTTGAACATTCCTATCAACTGGGAA GAGT[C/A]TGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTCTTTCTTTTGTAA TGCCATTTGAGGGATGATGTTTCTTAACTATGAAGTACTTGGCTGTCTCTCCATTCCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---	---	---	TCCCTTTATGCACCCAGAGATATTATTAACACCAATTAAGTAGCAGGCCATGGCTCATGGGACC CACCCOCGTGGCACTCATGGAGGGG[C/G]TGCAAGTTGGAACATATGCAGTGTGCTCCGGCCACACA TCCTGCTGGCCCCCTACCTGCCCAATTCATCCTGCCAATAATCCTGTCTATTGTTTCATCCTG GAGAAITGAAGGGAGGTCAGTTGTTTGTCATGATTTGTCAGAGAACCT
WI-7842	57 T C ---	---	---	CACAGCCATGCCCTTGAGGAGCCGGCCACCAGATGCTGAATCCCTATCCCATTTGTCGATGAG TCCCATTTGCCCTTGCAATTAGCAATCTGTCTCCCAAAAAAGAAATGTGCTATGAAGCTTTCTTTCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGCTTAGTACAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	---	CTGCTCATCACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGCTGCCATGCTCTGG AGGACAAAGGGGGCCACATCCCACCCAGCTGTACCCAGCCCGGGGAGGTGCAGCCCTTCCCTCC TGCTCTG[C/A/G]TCTGACTCTCTTTGAGGTCCCTGTATGCTACCTCTGACTCTCTGTTGTTCCCTCTG TGCTGCTCTCATCCATCTCTTACTGGGGCTGGGGCTTAGCCAA
WI-4767b	173 C A ---	---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGGCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGAGGTGGAGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATTCACCTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---	---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA/GIATTCATAAAGAGTT CCTCAGGCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGAGGTGGAGAGAGGGTATG TTTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACCTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGIATTAAT
WI-7718d	31 G A ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91	C G	---		ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248	A G	---		ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42	A T	---	C	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C]TGTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAA
WI-7227d	99	G C	---		AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTA[G/C]JAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G A	---		AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTA[G/C]JAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227b	93	G T	---		AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTTCATCTTTAGACAAGCTTTA[G/C]JAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A G	---		CCACAATGCTCTCCACGATGTCAAGGACTCCTGTCTGCTGGAGGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGTCTATGTTGTGATCTTCATCGAACAACATGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACAGGCCAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTTC
WI-7310b	234	A C	---		

WI-7310a	64 T A ---	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGGAGACAAGGAACCTT/A JCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAAACTGATCGGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCTCCCAATGCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTGTACCTGCCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCTCTGATAATGCTTGGGCTGATGCAATGGAGGGCAAAATGCGTCC CTGAGAGAAATCTGGGAGGAGCTGAG/GTGTGATGAAGGTGATGTTGGGAGGAGCACAGTGT CTGTGGGAGCCAGGAAGCTGCTCACCAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTGTACCTGCCCTGGGACTCCTATGATGGCCTG/C/GTGGTTGATAATAA TCAGATCATGCCAAGACGGGCTCTGATAATCGTCTGGGCTGATGCAATGGAGGGCAAAATGC GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGATGTTGGGAGGAGCACAGTG TCTGTGGGAGCCAGGAAGCTGCTACCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCTACCC AGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAGATC AGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTC/C/TGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTG/C/GCTTTCTTTCT ACGAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTTCCGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTG/C/GCTTTCTTTCT ACGAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTTCCGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTCCGACCCCTCATATTAAATAAGAGCAATGAGAGCGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGACCAAGAG/GA/GATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTCCGACCCCTCATATTAAATAAGAGCAATGAGAGCGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGACCAAGAG/GA/GATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC

WI-1795b	130 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGCTGGGTTCTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGT[C]C GTCTACCAATTTACCAAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGCTGGGTT[C]CTCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGTC GTCTACCAATTTACCAAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136 G A ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTCCACGCTCTCCATACGTAGTCTGGTCTCTCTATCACATTGCCA C[G]ATAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136 G A ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTCCACGCTCTCCATACGTAGTCTGGTCTCTCTATCACATTGCCA C[G]ATAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141 C T ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTCCACGCTCTCCATACGTAGTCTGGTCTCTCTATCACATTGCCA CGTAGC[C]TCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116 G C ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTCCACGCTCTCCATACGTAGTCTGGTCTCTCTATCACATTG CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52 G A ---	---	CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGCAAACTTCCAGTATCACT[G]ATATAATAATAA AAACCCGTGAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTAATTCAGTTTCTCAAAAGGAATATGAAATTT TGTTAAATGCAAAATCCAGCTGAACCTTTTGGACTTGCTTTTATTTCTT
WI-1126b	230 T C ---	---	CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATATAATAATAA CCCTGTAAAGTCTGCTTGCAATTTCAAGATTCAATATATATATCCAGATTGTTTCCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATAATTAATTCAGTTTCTCAAAAGGAATATGAAATTTGTT AAATGCAAAATCCAGCTGAACCTTTT[C]GGACTTGCTTTTATTTCTT

WI-1126a	97 T C ---	---	CTCTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATACTAATAAAAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTC[CAATATATATCCAGATTGTTTCCCGCAAGAAA ATTTTATTTCTCAAGATATAAAAAATAATATTTAAATTTCAAGTTCTCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACTTTTTGGACTTGTCTTTATTTCTT
WI-11183c	124 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGTGCTGATTTTAAAAATCTTTTAAACCTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTAAATATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---	---	TAGTGCTAATTTTGGAAAAGTTTGTGCTGATTTTAAAAATCTTTTAAACCTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTAAATTTCAATTTGTT ATGGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGTGCTGATTTTAAAAATCTTTTAAACCTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTAAATATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---	---	GCTTGGTTTGTCTTAGTCTTATTGTCTCAGTCTTGAGTCTCCCTTCTGCGTGGCCCTTTTGTATTCA CCCATACCTCTATGCCCTGCTCAGACCATTTCCCTCTATCTGGAGCGCTCTCCCTTGACTTTCTC TTCACCAACCTCTTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCGCCCTTTCC
WI-10770a	49 G T ---	---	GCTTGGTTTGTCTTAGTCTTATTGTCTCAGTCTTGAGTCTCCCTTCTGCGTGGCCCTTTTGTATT TCACCATACCTCTATGCCCTGCTCAGACCATTTCCCTCTATCTGGAGCGCTCTCCCTTGACTTTCTC CTGTTACCAACCTCTTTTATTCTTCAGGACACTCAGTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCGCCCTTTCC
WI-9667b	82 C T ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCCCTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATGG TTATCACTGGACA[C/J]AGCCACCTCCCGCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCAATAGGATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68 G C ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCCCTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATG G/CJTATCACTGGACACAGCCACCTCCCGCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCAATAGGATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

WI-10400d	189 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCITTCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCAGTGGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCAATTATG
WI-10400c	166 A C ---	---	ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCITTCCTTACCTTACTCTCCCAACCAAC/CJAAATAACGTAAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCAATTATG
WI-10400b	165 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCITTCCTTACCTTACTCTCCCAACCAAC/CJAAATAACGTAAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCAATTATG
WI-10400a	46 T C ---	---	ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTAAGATGGTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCAATTATG
WI-10809b	78 C T ---	---	AAAGGGCTACAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCA/CJTITAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGATGTATTAGCCCAAGGCGGTTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAAGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---	---	AAAGGGCTACAACTAAGGCCAAAAACCATGAAC/JTGGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCACTTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCGGTTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAAGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATAGTGTAGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAG AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CAATTTTATGAATATAAAGATCCCTGCAATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATAGTGTAGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAG AAGA/CJGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATGAATATAAAGATCCCTGCAATTTATGGTGTAGTCTGAGTCTGA

WI-7038a	31	G A	---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGG(GA)CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACTAGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGCCCCCAGCCTGGCCA GACAAGAAGACTGTGAGGAAGGGTCGGAGTCTGTAAACAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCTATTATGGTGTAGTCTGA
WI-3429b	64	G T	---			ATACGTTTCTGTCTGCCACAGTGAACCAAGCAGCCAGGTGGCAGGGTCCGAGTCCACAC(A/G/T) CCCTCAGCCCTTCAGCTTTCAGTGTGTCATGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAATACAGATCCCAAGTCTCCTCCTGGATTGGATCTAGCAAGACCAGACGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCAGCGGAGC
WI-3429a	62	C T	---			ATACGTTTCTGTCTGCCACAGTGAACCAAGCAGCCAGGTGGCAGGGTCCACAC(A/G/T)AG CCCTCAGCCCTTCAGCTTTCAGTGTGTCATGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAATACAGATCCCAAGTCTCCTCCTGGATTGGATCTAGCAAGACCAGACGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCAGCGGAGC
WI-6786c	151	G A	---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTAGCCCCATCTCT(GA)TGGGATAAGGTGTCATTTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786b	111	A T	---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGGA CCTGTAGCCCCATCTCTGTGGGATAAGGTGTCATTTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786a	106	A T	---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGGA CCTGTAGCCCCATCTCTGTGGGATAAGGTGTCATTTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6711b	226	G T	---			GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTTAACCTTCACTTCCATCACTCTGAAT TTCATATACCTCCATTATTAAATCAATACATCATTCGAGAGAAAAGACAAACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA(G/T)TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C	---			GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTTAACCTTCACTTCCATCACTCT GAATTCATATACCTCCATTATTAAATCAATACATCATTCGAGAGAAAAGACAAACGGTGCCAACTG GGTTTGGTTGGTGCCTGCACACCCACAGTGGCACTAAGTGAATCTCTAAA

WI-10613b	172 A C ---	---	---	ATTGTATGCCAAATCATAATACCCCTGCAATCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACAGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTG/C/GCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---	---	---	ATTGTATGCCAAATCATAATACCCCTGCATCTAGAAACATACAGTGTAAATAGAAATTTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACAGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTCCAAAGTGACTACCCCTTGAAGC ACATCCCCCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAAJA/ TJGGAATGAACCACTCCCTGCCATTTCCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCOCTCT TTCCACATGCCOCCATATGCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-7587b	81 G A ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTCCAAAGTGACTACCCCTTGAAGC ACATCCCCCTCTG/GA/JATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTTCCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCOCTCT TCCACATGCCOCCATATGCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-7587a	28 C T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCC/JTGAAGATCTGTGCTTCCAAAGTGACTACCCCTTGA AGCACATCCCCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTTCCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCOCTCT TCCACATGCCOCCATATGCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-10681b	103 T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCCTTTTAAAAAGCC/T/JAAGACAGCCATTTTAACTCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTCTTGGAGAGGAGTGACGCTCTGTAAAG
WI-10681a	41 A T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTG/JTTCAGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCCTTTTAAAAAGCCCTAAAGACAGCCATTTTAACTCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTCTTGGAGAGGAGTGACGCTCTGTAAAG
WI-7222c	126 G T ---	---	---	GCCTCTCCTCACTGCTGACCCCAAGGCTAGGAAAGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTGGGGATGGG/JAATAA AGGAGGGGGAATTCCTTGAACAAGAACTGGGGATGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGTATTTTGTGTAAGTGTATTTTCAAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGCGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGGATGGGAATAAAGG AGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGTTGTATTTCAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGCGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGGATGGG(GT)AATAA AGAGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTCAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTT(C/A)TTATCTCTCCAGTTCAAAATG CTTGCACTTTTAAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054c	237	G T ---	---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCCCACCATAGCCACTCTGCTTCC TGTCAAGCGCGCTTCCCTGGGCGTACAGA(GT)AATCCTTGCCCTT
WI-8054b	148	T C ---	---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAG(T/C)TTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054a	131	C G ---	---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAG(C/G)A CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-10854b	152	G T ---	---	---	TTCCACAAAACCTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAAGACGATAGTTAACGCTCTGGTAAGTTTAT ACGGGTGCGAGGCAACA(G/J)GGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTCTTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T ---	---	---	TTCCACAAAACCTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACA(C/T)GAAGACGATAGTTAACGCTCTGGTAAGTT TATACGGGTGCGAGGCAACAGGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTCTTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127 G A ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTTGGTGTGTTGACGAGTTGAGCCATTGTGACAGAGGCTGTAT[G/A]GCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCCTGACGGGAAAGTTTGTGATTCTAGATATTTAAA GGCAGAGAGATCAGAAGTGTGAA
WI-9826	125 A T ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTTGGTGTGTTGACGAGTTGAGCCATTGTGACAGAGGCTGTAT[G/A]GGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCCTGACGGGAAAGTTTGTGATTCTAGATATTTAAAAG GCAGAGAGATCAGAAGTGTGAA
WI-15986	60 T G GTGGTTTTT	TTGTTTGTGT GAAATGT	TGACATTATAT AAACGTAAAA	CGGACACGTGATATACAAATACAGATCGTATGGGTTTGTGTGGGTTTTTTTTT[G/J]TAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A G AG	AAC TGCAAAAT AGGAAACCAG	CCACCTGGGGC TTOG	TTCAGTAAC TGCAAAATAGGAAACCAGAG[G/J]GGAGCCCCCAGGTGGGACAAATCATGGCTACCCG TCCCAACAGAACAGGGGGAGGAGGTGGCCCCCTACACCCTTTAT
WI-8170b	259 G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAAAGTGCAATCCTATCAATCAGAA ATAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204 T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAAAGTGCAATCCTATCAATCAGAA A[T/A]AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136 C G GACA	CCTTTATTAAA ATTGTTTTCTT	GAAGAGAAAT GTAATACCTGT	CAGGATTCCTTAAGTCATCTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACTCCCTTTATTAAATTTGTTTCTTGACAT A[C/G]AGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56 G A TGC	TGAAATAAAA ACAATTTCTGT	TGTGTTGAAAT CAAACCTGC	AGCAGGGTTTGAAATTGATCCCTTATTTACATGAAATAAAAACAATTTCTGTTGC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83 C T ---	---	---	GCCTTATTGGGATTGCAAGCGTTACAAGTTAAAGACAAAAACCAAGCATGGGATTTGCCGGAAT ATTAGCGTTAAAGGAG[C/J]TGAGTTGAGTCAACACACGGG
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCTG TTCCCTAACCCAGCAGAGGCCCAACCTAGAACGGCCCTACCTAGCCCTTAAT

WI-8827	22 C T	TCCCTGGGAG TCTAGTGTTCAC	GGGATTAGGAT TTTAGTGTTCAC C	GGTGTCCCTGGGAGACTATGG[C]/TAGTGAACACTAAAATCCTAATGCCCATGCATTGGAATTATT CCGACTATTACTTCTTTAGTTCCTTCTATCCACCCAGCTCTCT
WI-8833	51 A T	TCTTCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCTCTTAAAGCTCTGTAGAGCTCTCTCCATGCCATCTCTG[A]/TJGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTCATAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTATGCCATGTTGGTAAAGTTTTCATGTTTTCAGTACATGGGTAAACCCAGGCCCTTTCCC[A]/GJT TATATCCAGGTATGCTACAAGTTCCTTTAACCTTATCAGAAAGTTATTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTGCTAATGCTCATTATTTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCT[A]/GJCCTGCCCTGGCTTTGGCTCGCTGCTGTTTTTGGTTTCTT TCTCTTCTACTGGCTCTTCTTTGCTTTGCCAGCCACTATGCTGCTGT
WI-8853	79 C T	CCCGGGCATTG AGGATA	AGTCTTCTGTA GCTTCCAT	ACTTTTCTGAGCTGAGCAACCTCATCTTTAGCTTCTGGTTGATAACGGCTGTTAATCCCCGGG CATTGAGGATA[C]/TJATGGAAGGCTCAGGAAGACTTCTATCTCAA
WI-8865b	52 A G	---	---	AGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T]/GGTGAACAAACACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTTCCATATAAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T]/GGTGAACAAACACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTTCCATATAAA
WI-8895	32 A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAAAT[A]/CTCCCGTCTTTGAAATTTCCATTAAAGACA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAATAATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G]/JTATGTCAAGTTAATAAATTTCTAAGTGTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAAACAGTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTGCTGCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATGAAA ATTATATCTCAAGTAAGTCAAGCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAAATGCTGCCAATGCA[A]/GJTATAGTATAGAAATAATACGCGAGCTGTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATG AAAAATCATATCTCAAGTAAGTCAAGCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAGACACAAATGCTGCCAATGCAATAGTATATAGAAATAATACGCGAGCTGTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A]/GTCCCTCTGCGCTTGTACCCACATCCACAGAGCA GCOCTAGTGCCAGGTGCAGCCACTGCCACCCACGGCACACGGGAACAGGCCATGCTGCTGC

WI-12108	40 C T	TGAAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTCTGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29 G A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA GG	CAGGCAACGGTCCACAAAGGTACAGGCA[GA]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCTCTAAAGAGACATTTCTCTTAGAGATTTCATTTTAGTGATCTTTAAAAAAAAT CTTGITTAACCTGGCTCCATCTTTTCTGGGTGAGGACACC
WI-12201	61 C T	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTGGAGTGTTATGTCCCAAGCCCACTGATCACCTGCATG[CT]GCCA GGTATGGTGGGGGTGATGGACGTGGGTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31 A T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCAGCCAGCTCTGACTT[AT]CTCTCTGTTCTGTCATCTCTCCCCACATACCA ACTCTTCACCATGATGATTATACCAATAATACAGTTTCTTATATAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G	TGGCTCGCTG CCTC	AGGGATCAA GAGAAAGGC	TTTTCTGTTTGAATGATCCGAATGCTTGAGAAAGAAACCCCTGGCTCGCTC[AG]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGGG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAAT	TCTTTTCTCTTT TGGTAGTGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTGAGTTTCTAACCCAGCTGAAAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTTAA[AG]CCACACTACCAAAAGAGAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C	GTTGAGTATTT GTTCTGCTCAT AATT	GGGAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATATTCTGATACAAATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATTT[CT]CCAATATGTACCAGACCTTCCC
WI-12326	25 G A	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[GA]CTTCCAGAAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCATTTCAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTTCAGCATATGTATTAT[CT] TGAATAAATTTACAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T	CAGACACAGC ATCACACCA	GACCTTCCCGT GGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAGGGAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[CT]AGGGCCACCGGGAGGGTGGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67 A G	GGGAGGAAAA TCCAATAAAT TTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAATAAATTTTAA[A/G]AAGGTTTAGCTATTTCCCAATGCTATTTAATACAATTTAGGTTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40 C G	GGATAAATCA TGTCOCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCTTTATGGATAAATCATGTGCCCCA[CT]GAGAGCCCCAAAGCTTGATGACAT TCTGTAAGTTACAAAAATGTATCTGAAGAGTTATCTGTTCTGCC

WI-11352a	69	T C G	AGCAGACAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTTCCAGAAAGGAGAGAGAGTCATCTACATAAGCACAGCACATAGTGGAA AGT[C]GCTAAGTGTCTCTACGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCCCTGA GCAC	TTAGCCCCATGCTGTCATTTGCAATCACCTGTGAACCTATGAAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTCA[C]TGTGCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGT GATTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAGACTTTCATATTCTTGTTTTTTAAAAAGTC TCTTCAGT[C]AGGAAAAAGCTACAGATTTAAAAATATGACCATGACTAGATAAGATCAGC
WI-11388	88	C A AAGTTC	TGTTGAAAT ACACGTAAC	TGCCTGTATC CAAGTTAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAAGAAATGAATGTTTG AAATTACACGTAACCTAAGTTC[C]ATATAATTTTAACTTGGATACAAAGGCATTGTTATGCTAAT
WI-11392	55	T G ATAATAC	GGTTATGTT CTTGAACCTTA	GTACATTACAG TGTTTTGTAAA	TTCTATCATTCCTAAATGAAATGGCAGGTTATGTGTTCTTGAACCTTTAATAAATAC[T]G[C]TTTTTACA AAACACGTGAATGTACTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTGTGTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAAATAGATGGCATTGTTTGTGTTTGTGTTTGAATGGTGTTTTATGTTGATGGGTGAATA TGAAAAATAGCTTACCTCATCCACTCTAAAGGTAGTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100	C A CAGC	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTCAGTCTTCCCCAACTAAACCGTGAGTTCOCAGTATGCTGGCAGCACGTCGTCTGTTCTTCTGGTG TATCCCATTAAGTGAATCCCAACCAACAGC[C]A/CAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T TTTATTTGCA	TGAGAAGCCA CTTATTTGCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTATTTTGCAG[C]TCTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACCTTTCTATTATCTATTTATCTCTCACATACATTT CATGTATCCCTG
WI-13364	35	A G	TTTTCTTTTGTGCTCTTTTTTTTAGTAGAAGC[A/G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAATGTCA
WI-11276	41	A G AGCAGAC	GGCAGCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATTAGCCGGGAGCCAGGAGCAGAC[A/G]ACCGGCTCCTCAGTACACATT CCCCACCCCTGCTCGGTGCTCCCACTCAGGCTGGGCATGGAGGGGCGAGGTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAACAACCTTAATAATTTGCACTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACA CTATTGCAT[A/G]GGAACAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	AATGGTCTGGTTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGTACAAAATTACA GGTGGTTTAGTTCATTACATG[A/G]TACAAATCATTTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52	C T A	GGTCATTGAT GGAAAGACAC	AACAAACCA CCTGTAATTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTGGCTATAGTCAAGTGTCTAAAACTTGAGCTTGAAGAGAACACTTTGTGGGCTT[A/ G]TTCAACATGGACTAGTATAGTCCACCCAGATTCTAACTGGGTAGGCTGGGGTG
WI-12345	37	C A	GTGGCAGGAA AAAGAGGAA	TTCAGAGGGG TTCAGG	GGAAACAGACCTGATCCAGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTTGCAAAA
WI-13416	71	C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCATGAATA ATTCAA	GAAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAAGTTTTTTCAGAAAAAAATAAAATGACAAGAAC CATA[C/A]AAATATTGAAATTTATTCATTTGAACATAAACACTTAGCAGAGGAAGGACTTTTGTAT
WI-12310	46	G A	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGTCTT AAA	TTTGAAAAGATGCTGAATTTATTTCCCAAGTATAATTTTAAAGCT[G/A]TTAGGACCCAAACATA TTTAAACATCTCTACACATACAGAATTTTCAAGTTTACAAATATTTCCAGAAGGCAATTTTCTTAAGCAG T
WI-12086	72	C T	CCGGGAAAC TTGGATT	GGAGTCTTCGG GTCITGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAACCTTG GATT[C/T]CCAAAGACCCGAAGACTCCTCCAAAGTCTCACTGTTAGTAAGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T G	GGCATAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCCC	ATGTCTTACAGGTTGTAATTTGTTAAGAGTTGTCTATCTAAATTTTACATAATTTATGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTTGTACAGACTTTTCTCTC
WI-11585	79	T C	TGGGTTTGCA AAACAAAA	CCATGCTTCAC TGATACTCC	TTAGAAGGAAGAAATAAAACACGGTAATGGGAAATTCAGTTTCAAGGTAAGGAAGCTGGGTT TGCAAAACAAAA[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G C	---	---	TTAGTTGGTTTCTCGAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTTT G/CJAGAACTAGGAGCTTTTCCATGAAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C A	---	---	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACCTGTGAACCTGCA[C/A]ATATTAAGTATTGTCAGCTAC GGACTTCGT
WI-11614a	60	A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCACCTGTGAACCTGCAACATATTAAGTATTGTCAGCTAC GGACTTCGT
WI-11626b	83	T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAAACATGAAGGTAGGGATAAGTGTACAGGATAATATATCTACAG ATATTTTTTAAAAATAAAT[C/T]ACTTAAATAAAGAAATTAGCCATACCACATTTGTTCCATTGCTAC AAGAACAAATGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTAAGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAG[G/A]GATAGGTGTACAGGATAATATACT CAGATATTTTTAAATAAATTAATTAATAATAAGAAATTAGCCATACCACATGTTCCATTGCTTAC AAGAACAATGGCAATGA
WI-11627	23	T C	CCTTCCCTTC ATTGTCTC	CATTGCAACC CATCTCAAG	ACCCCTTCCCTCCATTGCTCTC[T/C]CTTGAGATGGGTGCAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGCTGGCTTACTCCATTGCGCATGTCAAGTCCATCCATG
WI-11636	61	A G	GGACTTAAAA AGATCTGCTTA G T C T	AGAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCTTA[G/TA] TATCCACATAACTCTAGTGTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA T	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAAAATAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCAT[C/G]ATAATCATCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C	GCCAAAAGAC TATTCAGCAA C T G	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTTCAGCAACTG[G/C]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATACTCTACTCAGAGTTCACACTCATATTTTCATATTTT ATTTTGGGTGTGGGT
WI-11656	28	G A A A	ATTGATTTTAG AAGGAAGTGC A A	CAAGGCTTTGT CCTCAAGTAA	ACCTGATTGATTTTGAAGGAAGTCA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGSCAGTTGTTT AAATGTCTCTGAACAATCAGATTCCAGCCTGGAT
WI-11680	55	T C	---	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTTCTCCCTTTT[C/CT]TGCAAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAGT[C/A]AGGTTGGCTTCTCTA ATGCCACCATCTTGTTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA T CAGCAG	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGTGACATACTTTCAATAATTAATAATGAATAACTGAAATAACCCACAGC AG[C/TT]TTCAGTAAATTTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTCTGCAGA
WI-11706	60	C T	TGGCTGGAATT TTCTCTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAAATTTCTCTTCTGTACAAATTTATTTGC[C/TT]GGCTG GAATTTGTTCTTTGGTGATTTGCCCCCTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTCT AATTTACGGG A	AATATCATCTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAANA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACACAGCCAGCCACACTCTAGACAGCCCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCAC[C/A]CTCCTCCCTCTCCACACACTCCTTC

WI-11715b	123 C T	AGCTGGCTGC AGCTT	TCCCCATCCTG TGGCT	AGATGGAGCTGTTGGGAGGACATGCACACAATGTAAACAGACAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC AGGATGGGACTGGGGAAGA
WI-11715a	49 A C A A A	GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGATGGAGCTGTTGGGAGGACATGCACACAATGTAAACAGACAAA[AVC]TGCAATTACAACTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTACGCCAC AGGATGGGACTGGGGAAGA
WI-11727	43 G C T C A A C A	AACAATCCTT AAACAACATA	CCTGTGTTTG TGTTGCAG	CTGGATTCCTATACCTAACAAATCCTTAAACAACTATCAACA[G/C]CTGCAACACAAACCACAGGC AAATGAAACAGATGCCCCAGACAGACACCCACCACATGGCACAC
WI-11728	16 C G ...	ATCTGTGGTTT TCGCCCTG	---	TTTTATTATCAAACT[C/G]CAATTCATTTTCAAAATGTAAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTTCTATCTCTTCCCACTTCTCTCCCTACAAACCCGGTTCCAAA
WI-11758	61 A G T C G C T G	GCCTCACAAA GTATTTCTAA	TGATGGCCCT GTGGTCTA	TTTTCTCTCTTTTAAAGTCCGCTATACCTAGAGGAGAACTGTGGTTTTCGCCTG[A/G]TAG ACCACAGGCGCAATCACACAGCTTCTGTAGAGAACATGGAGTGCCAAAGATCACCATCA
WI-11295	37 A G A A T A T A A	GGCTCACAAA GTATTTCTAA	AAAGTGCTCA TCTGTGAACCTC T	COGGCTCACAAAGTATTTCTAAATATAATTTGCTT[A/G]TAGAGTTACAGATGAGCACTTTTCA CATTAGTGATATGCAACAATCACTATTGGCTCAGCAGGAACAGACTTTT
WI-11773	93 T C ...	GGCTCAGAGA GCAAGGGA	---	AGCATGATATCTGCCTGGAGTTTCTGTGAGCTCAGCAACACAGAGTCAGAGATTAAAGAATT ATTTATGCCTCTTTTTTCCCCCT[C/G]GTGATTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G G C A A G G G A A	CCCAACTTACC GAAACCTCTG	AAACTCAGA CTGTAAATTTT GTGTG	CATGACAACTCTTTTATTTAATGGGCTCAGAGAGCAAGGGA[C/G]CACACAAAATTTACAGTCTGA GTTTTGCGGCGAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G A A C C T C T G	TCATCTAATCT GTGAGGTATTT	CGGTAGGGAG GCTAAGC	TAATTCACCCAACTTACCAAACTCTGT[A/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A A G T A T A C A	GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TTTTAATTCCTCAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTAGTATACAG[C/A]AGT GATTTCTCTCTTCTCTTTTATAAGTGAAGAGGTTCAACTATCCAGACAGTCCCCTCTA
WI-12469b	91 C T A A G T T T A A A	GTATTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTACTAAATTTCCATTTCTCCCTTTTATAGTTTTTAAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTTCTA[C/T]TTGACAGCAGAGTCTTCAAAGTTTGTATAGACAATCTGA AAATGGGTTCTGAAC
WI-11906	52 A G A T C T G A A	TGTTATAACAT CAAAGAAAGA	TAAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTTGTGTTTAACTCAAAAGAAAGTCTGAAT[A/G]TGAGGGAACCTG CAGAAATTAACCTTCAGTCTAATCTCAGAAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTTGTGTG GGTGGTCAAG[AG]CTATTTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCAGCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[TT]G[GT TTATTAGTATATAAAATGGCTTTACAGGAAGCATTTATGG
WI-11946	31 C A	CCCTAGTGAATACAACCTTTTGTCTGGAGAC[C]CAGCAGTGTCTAAGAAAACCTCCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTCTTGGCTTGAAGATCAGATCTCTGGTTTATTTAA[TT/ G]ATCAACACTTACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTGAAACTGCAGAAAGGGCAGGACAAAACAATCAGTTTCTATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[TT]AATAAAAATACTGTAAACACATTTCTCTCATTTCTCTTACGA ATACTTCTTTTGTATTTGCAAAATCTATGGCATAACAGAGGCACCTCCTCAATGCCCCTG
WI-11049	95 C T	TTCTGCTGAAGATCACAAAACAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTGTACCTTT GTGTTATTTTCTGTTTCAACTAAGGAC[TT]AGACTTCAGAAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTTCATTTGTAGGAAGAACATTTCAAAAGCCCCAA
WI-15488	69 C T A C	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGTTAGGAAAGTTTCTCACTCTGCACATATAAAAGGACAGCCAGATATCA AC[CT]TTGTTACAGAAATGAAATAGATGGAAAATTTTAAACAAATTG
WI-13654	49 A G C G T	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAG TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGT[AG]GTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAAGGAGCTAGGACAAATTCCTTGCCT TCAAGTAAAAATGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAGTA C[CT]TGTGGGGTCTGATGACTTCCACGGTCACTGGGGATCCACAGAGGGAA
WI-11070a	110 G T T	CAGAAAATCA GCCAGCTATCT	TTGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAAGGAGCTAGGACAAATTCCTTGCCT TCAAGTAAAAATGTGACTGAGCAGAAAATCAGCCAGCTATCTTGTGGTGCAGAGAGGTACTCCAA GTACCCGTGGGGTCTTGTGATGACTTCCACGGTCACTGGGGATCCACAGAGGGAA
WI-12020	121 T C	AATCTTTTATATTTCCAGCTGTTGAGACAGTATTTTGAAGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAAATGAATACATGACCATTT[CT]CTCTTTTAGC ACGTTCTTTGTTCTCCTC

WI-11076b	142	G A ---			---	CATGGTTCTGCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGATTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106	T C AGGCA	AAGGGGAGC	TOCTGCTCTGG GTATGTGAC	GGTTATTCAAA AATTAGTATGG GACA	CATGGTTCTGCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCA[T/C]GTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGATTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA	CGCAGAAAAA			ACCTTTAAAGTTTCTCCCACTTACTCCCGCAGAAAAAGGCATATTCAA[T/C]GTGCCATACTAATT TTTGAATAACCTAACTCTCCCTTTTGTCTTCTACTAAGAGAGTTCTTTTGGCTACAAGTAACA
WI-14267	28	T C ---			---	AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAAATGGGAAGGGGAGGTTAGAGAAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAGTATAAAACTOGTA
WI-13892	50	G A TAGAAC	CTTTTCATTTT TGCTTTTFAAA	TGATGATGTCA TATACTAAAA ATCAAAG		GATTTGTTTATTCAATCTCGCTTTTTCATTTTGTCTTTTAAATAGAACA[G/A]CTTTGATTTTGTAGTA TATGACATCATCATGATGAATTTTCTCTTACTTTGTATTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGATGAGTTCA
WI-13951b	88	G C ---	CATGAGAGGA	AAAAGCTTCTT TCCCTTGA		ACCTCTTCTGATGACACTGTACCTGTAGGGGTCTAGAGAGAAAGTAGTAGACTCCTACTTTGC TACAATTCAGGATGCAGGGCATGAGAGGATCCCTCTCTC[G]TCCAAAGGAAAGAGCTTTTGGC
WI-13951a	39	C T CAAAA	GGAGTGAACA AAGTAATGAA			AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAAGAGAGAGAGAGAGAGATG GCCTTCTTGTAAATCTGGAGCA[G/C]ATTCAAGCAGCAATATTTACTGAACACTTGCTATGTGCTG G
WI-13264	25	G A TTGCCCAT	AAAAGGCTC	GGAGGGAGAG ACGGGAATA		AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCAAGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAAATATTTACTGAACACTTGCTATGTGCTG G
WI-13960	39	A C TGATAGA	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT C		GAGACCAAAAAGGCTCTTGCCCAT[G/A]TATCCCGTCTCTCCCTCCTGACTGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCATGGCATGGTGATCCCTCTCTCTGGGATCTGTGAATATAACCA ACTGTCTTGTCATGGC
WI-15843	62	C T CAG	ATCTTATAACC AAGAAGCCTT	CTCTGGCTCAG ACTTGCTCT		TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[C/G]ATGCAAAATTTTGTCTTTCATGCA TTTGTGGAGAAAGTACTAATTGTTCACTGTGATTTCCCTCACAAGGAGTTGAGCCCCCTAGATGAC AACTCTTTATTGTTTAGCTAGCCCCAGTGACTTTTATGCATCTTAAACCAAGAGCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACATTTGTCTCAGGGTCCACAGGAACCCAGGTCTTGGCT

WI-13983	52	G A	TCTCTCCACT CCTTAAACCT	CAATACTCTCT TAGCCGAGTGG	TTGTGTACTGATTTCCGAAACATAGAAATCTCTCTCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACCTCACTGACTTAACAGAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGAATAAATAAGATGGACTTGCAGGTGTAAAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCTCTGAT[G/C]TTTCCCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCAAGAAAGGCCCGGAAATATGAGTGAGACTCA
WI-14284	55	C T	---	---	ATTTCAAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGAAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCCTTC ACCAAATCTT	ATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATACCTTGGTGGAGGGATA CCGCTGCTATTCACAGAT[G/C]AAGATTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT ACAAC	CATAATATTG AAGTCAGTGGT TCTC	TTTATTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACCTGACTTCAATATTATGAGAG AAATTAATCCAGGGAATTTTGCAGAGAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG TTACCA	TCTATACACTT CTCACTCTCTT GCTT	AAATATGATTCCATCCACAACATTTATTGAACAGTTACCAT[C/JAAGCAAGAGAGTGAGAAAGTGT ATAGAGGTGATTAAAGAGTGTCCCTGTCTCGAGGGTTTATAGCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTACGAAAGGACTCTAGAACTTGAGCA ACA
WI-13536	29	T C	---	---	TGAAGGATACAGAAAAAACTCAGCGAAGT[C/J]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A	---	---	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AAGTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACCGCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCCAGAGCT
WI-13477b	61	A G	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTGTTTTTTCATTAGCTTGTCTTCAAA[G/G]GAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[G/G]CATTGTTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86	A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTTAGCATGCAATGCAATTTATTTCTGGCAATAAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTTCCAAAG[AT]AAATGTTTCTGAATGTGCACACTAGAAATATATGCAGAATCCCTTT AAACAGTCGACT
WI-12229	89	T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[AT]GACCACAAAAATTAAGATTTTTTGGGACAATTCACATGTTT AAAT
WI-13582	43	C A	TGCAATCTAG	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[CA]TGGAACTCTAACTGGCGCAGAG AAATCAAGACCGATGGTGTGAATCTGGGGCAGCTTCAAAATTTCTGCCTCTAAACATTTTCAC CCAAITTTTTCATTATTGCC
WI-13857	28	A G	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG]TACATTTTAGGTATCTGGCACAAATTAACCAATGT CTGCCCATTTTGTGTAGCTTTCATACAGTACAGATTTCATTTGATGTCGCTCCACATCTG
WI-15809	77	T G	TGTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[AT]GTTTACAAACATTGAATAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123	A T	---	---	TTAATCAGTCTGTGTCAGAAAGAAACAGGACTTGTATCAAGCTTCCAGCCCTCACACTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAAGAA[AT]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81	T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTTCCAAAGATGGGAAGCGCATTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACTTA GCTGCAGTAACTAT[AT]GTCATCCCATCCACTCTTCTCTCTTTTGTGACTGAAACTCTTCAAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24	G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAATG	TCITTTATTTCCAAAGATGGGAAGC[GA]CATTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAACTACTGCTCATCCCATCCACTCTTCTCTCTTTTGTGACTGAAACTCTTCAAAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59	T C	GGCTGGACACT GCAGTGAT	CCACACCTGC CCCT	GCTCGTAAATGAGACAGAACGCTACAAATCTGTTCAACACTGGGCTGGACACTGCAGTGA[AT]CJAGGG GCAGGTGTGGGCGAGGTGGGGCTCTGAGCCGAGGACAAATGTCATGGCAGAGCTTCCAGAA
WI-13578	48	T A ACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TTTTTTTTTGGTGAGTGTGTTCTTCAATAAAGAGCAGAAAGAAACC[AT]AAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTTGATATTTTGTCTTTTCCCGAGGGCAAAAAAGA GAGCTTCCCAGAAACCTC
WI-13789	62	G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAACCTCAAGAAATGGATGGCTGAGGGAG[GA] GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCTCTCTT GAGGTCCCT
WI-13594	66	G A AGC	TTTTTAACACA GATCACAAAA	CCTTTGGCCCA GTACTTTT	AATAACAAGTTTAAAGTTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACAAAAAGC[GA]TGACAAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T	---	---	GTTCCTCCACCTACTCCCGCAGAAAAAGGCATATTCA[C/T]GTCCCATCTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACGAG	TCCCCACCCCA COCT	GTCTCACTTCTGTCTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGIGATTGTGGCCACACT GAAGACTCACGAA[C/G]AGGGTGGGTGGGAATACCTTAATCAATATTTGTGGAAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACTTTAATGAGCCAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTAGGGAAGAGCATAGAGACCACCATCAGCAACCCCTCT TGATTCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAA T	GATAGGAAGAAGAAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[C/G]AAATCTATTAAATTTAAATATTGTCATGAGGTATGCAOCT GCCC
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTCAATATTTTAC TTTTAAAC[A/T]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAGATAAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAA	CAATACATTT GCATTTTCTTA	CATGATACCAC AGTTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTTGCATTTTCTTAAAA AAAGAAAGACATTT[A/G]TTACAGAGAAACTGTGGTATCATGCAAGAAAGCAGAAAAAATTT
WI-13909c	93 A T	---	---	ACTTAACTGGCTTATCTCACGGTAATCTATCTGTATTTCCAGTGAAGTTCACTTCTCTCACACT CTCTTCAAACTCGAATATCTTTTTC[A/T]GAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC T	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTCACGGTAATCTATCTGTATTTCCAGTGAAGTTCACTTCTCTCACACT CTCTTCAAACTC[G/A]AATATCTTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	---	---	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAAACAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCAITCTGGAC[C/A]ATGGGAACCTTGAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78 T C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAAACAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCAITCTGAGACCATGGGAACCTTGAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTCTGTTTGGAGACTACCATTTTCAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[C/G/A]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCTTTTGTGCG/GA/JTTTGAAGACTACCATTTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAGTGTGGGAATCAOCTCATCTGTGC
WI-15747	88 T C AGTGTT	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAAGTTCATA TAATTT	TGTAATCTGCTTACAGTCCCTTTGCAAGACAGACATATGTTTTGCATAAAGATATAAATTGCTTCAT TTTAAACTAATTTAGTGTTC/C/JTTTAAATTAATGAACCTTTGGTGAATTAATGAAGTGTACCAAAAC C
WI-13752b	117 C T ---		---	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCAGATGAGTTCTCTCTGTTAAGTCTGGATATACTTGGCTTGCA/C/JTGGACACCTTTTACG GAGGATTCCGGACAAC
WI-13752a	106 T C AGTGCTGA	CCTTCTCGTTA CAGTACATGA	CCCTCCGTAAA AGGTGTC	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCAGATGAGTTCTCTCTGTTAAGTCTGGATATACT/C/JTGGCTTGCAOCCGGACACCTTTTACG GAGGATTCCGGACAAC
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAACCG	AATCATTAAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACACAGTACATGATTACT/J/GCGGTTTCCAGAAATCTGGATAC
WI-13744	115 C T AAACTGAA	TGCTGCTGAAC	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTTCACAAACACACGTAAATGGAACCTTCATGCAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGATGTTGGTCTGAACAAACTGA/C/JTGTGTGCTTATCTTTC CTGATTCT
WI-14061	68 C T ---		---	CCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAGAGAGCCCCCGTACATACCTTAT C/JTJAACCATTTTCATCCACCACTTTGTAAATCTCATCTCTGGGTCTGGATCTCAAAAACAGAT
WI-15719	69 A C CATTGAGC	ACCTTTTCATC CATTGAGC	TGATACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAAACACTACCACACTGAATATACTGAATTAACCTTTCACCCCTTTTCATCCATTGAG C/A/CJAATTTAAACTCTTGCCAAGTATCATGAACCTTACGAAAGAGGAGATAAGAGATCTGATC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAATCAACACATACATAGATCAAAACAGAGTACCACAGTATGCTTTATTTTGCA GGTATTAAATGGTCTCTAAATCGATACATCCAAAACCTT/C/JAGTTAGCAGCAAGCATCAGTCTCTTC
WI-15736a	27 G T CACA	ATTTTATTCAC ATTAAACTTG	GTTCTTTTGATA TGTTGCTTAGT TTT	GGATTTTATTCACATTAAACTTGACACA/G/JTJAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72 G A ---		---	TCAAACTGCACACTATAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTGC/G/JATAGTGACACATAGCTGTACACACAGTG
WI-13785c	56 A C ---		---	TCAAACTGCACACTATAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGAC/JA/CJCAAATG AACAAAGTGCAGTGTGACACATAGCTGTACACACAGTG

WI-13785b	40	C G	---	---	TCAAAGTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG
WI-13785a	27	T C	TGCTT	---	TCAAAGTGCACACTATAAAAGTGCTTT[C]AAATGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG
WI-13793	88	C G	ATAGG	GGGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAAAATAAAATAGTTTTTACCCCATTTGATACAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCCTGCCATAAATCTATGACTTG
WI-13794	52	A G	TTTCITTC	AGAAATGGGCTC TTAACCTTGA	TAGTCTCCTACAAATTCCTTCAATCCATTTTCTCTCCACCCCTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCAATCTTCAAAACAACAAAAACAACATAGAGCAAT
WI-15729	35	A G	GTGAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACITTTGAACCATGTGTAGACTGC[C/G]AGGCACITTTAGAAAAGAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAGGAAGGGTAAGTCCCTGTTTGACGCCCGGGCTGCTCATTTGTTA
WI-13424	66	G A C	ACCTATTC	TTTTCTCCCC AGGGTCTA	GTCCITTTGCACAAGTCTCCCAACTGGTTGGAGTTTCCCTCTGAGGTTTTTCAACCTATTCTT[C/G/A] TAGACCCCTGGGAGAAAAACACATGTGTAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T C	AATT	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGAGAGGCAATTT[C/G]GAGATCCAGATTGAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTAATCCTGAACATCTTGAAGCACGAA
WI-13446	22	G C	TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACATCATCA[C/G]CCTTCTGATTTTGTATCCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTGAATACTGTTTGTGAGAGTAGTGAGCCCTTTTACITTTTTT CTGACTGCCTAAT
WI-13725	56	A C	TGGGTGOC	OCTGTGTCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/G]GCCCGAG ACAGCAGGATAAGTTTCAAAAACCTTGACCAGGCAGGTTAGAACGAAGGCATGGTTCAAGGATG
WI-15702d	107	T C	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAAAT[C]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T C	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/T]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C T	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/T]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C A A G	A A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T A T G A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G T A A A G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A C C C T G T A A C A A T A C T A A T G G G T T C T T T G A A C A A T A G T T T
WI-13831b	113 T C		---	T G A T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G T A C C T C C G G T A A G T T T C C T T C T C T C T G T A G A T [C/G] T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A C C T C C G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A		---	T G A T T G A G C T T A G A A A G G A A G T C A T G T T G A A A T C A G A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G		---	C A C A T T T C A G C A A A C A A T C G A G G T G C A A A C A G G G T T A T T T C A C A T T A A T A T A T A A C T G G A T T T T T T G T C A A A T A A T A G G G A [A/G] T T C T C T T A A A T A A C C A T C T C C T C A C T T C A T G G C C A G T
WI-14373	95 A G		---	A G G C T G T T T T T G A G G C C T G A G A C C C C A A C A C A T G A C A A C G T A A G A C T G T A A C C A T G T C A T G T A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T	A A A G A A G T A A A T T A G G A A G A	T G T G T C A T G T C T C T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G	C A T T T A T T T T G A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G G A G G C C C T T T
WI-12169	121 G C	A A T A A A A C T T C C T A T T T C T T	G G G T T C T G A G G T G A A A G A A A A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T C A T T T C T A A A T T T T C A C C T T T A T T G C T A A G T T A A A A T A A A A C T T C C T A T T T C T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T O G T C A A A T A C T C T	T T G T T T T A T T T G G G A G A A T G A A G G A G G A G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T G A C G A C T A C A G C T C C T C T C T C T T T G T A C T A C G A G A C C C T G C T T A T A G C C C C A C A G G A A A T C C C T C A T C T G G G T T G C C A G A C A G

WI-14379	102	C T	CAAC	GGGTATGTCA	ATCATCTGTT	TTATGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAATATCCAATCCTAGTATGATTTCTTT TACTTGCTCTATTAAACAGGTTATGTCACACC[C]/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C]/A]CCACCATTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	---	---	---	ACCGCAGAGCTGCTGATTTAA[A]/A]JACAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTCCACCACCCC
WI-15937	24	A G A	GCAGAGCTG	CTGTATTTAA	GCAGAGATCCA	TGAACTGAAACGATTTCTCTCCA/C]JACACCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGGCGAAAAAGGAAGTTTCAGGTGATACAAGATGCTCCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	AACTGAAAC	GTATTTCTCC	GGCCTTTAAGT	ATGTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A]/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACAAAGCTCAGTCACTAC
WI-14124	92	A G	---	---	---	GACAAAGGCGAGTTTCTGTAGTCCAGCAGGGCCAGAGCAGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTTCAGCACTA/C]T]GTGGCCATGCCATTCTGTAAAGTGAAATTAATGAACA
WI-14125	88	C T	CATAGATTTT	GGTTGACCTG	GGATGGCATG	GTTATTTTCTCACAGTCTGGAGGTAGAACTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGCTTCACATG/A]GCCCAAGAGAC AGAAACAGCTCTCTGGT
WI-14136	120	G A	ATGCTTTCACA	GCTTCTCACC	CTTGTCTGTC	TTGTTGTTGGCACCAGAAAAGCT[C]/TATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-14138	23	C T	GAAAAGCT	TGTTGGCACC	GTGACATAACA	GGCAGGTTTATTCATAATTTTCAAACTTGGAAAGCAACCAAGATGCTTCCAGTAGTAGTATATCA GACAATC[G]/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74	G A	GACAATC	TAATATT	TAATATT	TTTTTAAGAGTGCTCTCACATCATTTATTTGATTGTCACACAAACTTTTTTAACTC[C]/T]GTCAA AAACAAGAAGACAGATGAATAAGGAAGCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCG
WI-15953b	59	C T	---	---	---	TTTTTAAGAGTGCTCTCACATCATTTG]TATATTGATTGTCACACAAACTTTTTTAACCTCCGTCAA AAACAAGAAGACAGATGAATAAGGAAGCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCG
WI-15953a	26	T G A T	TCCTTCACATC	TCCTTCACATC	TCCTTCACATC	TTTTTAAGAGTGCTCTCACATCATTTG]TATATTGATTGTCACACAAACTTTTTTAACCTCCGTCAA AAACAAGAAGACAGATGAATAAGGAAGCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCG

WI-14631	82	G A ---	---	---	TGAATTCATGACAGTTTTGCCTCTGTTTAGTGAAACCCCTCACAAGCACTCTGCATAGTCCGCTTTCTGCTCTTTAAAC[G/A]TGCTGGTCCCTCTGCCAAACTTTTAGGATTGGCCCTCCTCAGGGCCTTGCTCGA
WI-6053	24	A G ---	---	---	ATCACCACCGTGTCTAAGAACAAC[A/G]JCTTCATGTCCAATCATATCCCGGGACTTTGTCAACTGCAGTACACTCTCGCAATTGAACCTGGCTTCTCGAGGGAAAGCCTCTAGAGCCAGGTAGGGGGTGCAGCAGTGGGGTATACTGGGCTGGCCAGTTGGAACCAACGGAG
WI-15964	99	T A CTGGAGGTA	GACTTCTCCAC	OCTCTTGC	CAGAAACCTCTCTGTGTTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTTGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT[A/G]CAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103	G A GGCAC	AGCAGCTGGG	CCCCCTCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAAAAGCCAGGCAAAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGGGGGAGGAGCCT
WI-12179	96	G A TGGAGGTCA	GGAGGTACGG	TCGAATGACCC	TAATTTAAACACGCCCTTCCACATAGTGCCTGAGGCACTCTGCACATTTCTCTAGAAGGACATGATAGTGATGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	CAAGAATCAT	GGAGATATTGA	CACAAATAGTGAAATTATCTGAGCAAGAATCATCTCATTTAAATTTG[C/G]AAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105	T A ---	---	---	AATGTGGACTTTCAACAAGGGTTTAAACTAATCTAATACTTCTACAACACATTCAGAGCATTATAACAAGAAATTTACAGGCAGCTAATGTATTAAAT[A/A]AACCATGAAAAAGAAAAAATCTGATCTAGATGTACAGAAATGGGCTGAGACTG[C/T]TGCTGGTAGATGCAGTGTGTGTATGTTCTAC
WI-13473	31	C T ---	---	---	TCATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAATGTTTATATCACAGTC
WI-13967	103	A C AAATAAAAA	AAAAGACTAC	TTGTGTTTCA	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAACAAAGATAAAATATGTCAATTCAGCAGTCATTTAAAAATAAAGACTACAGATACAAGGAAATAAAAA[A/C]CACTTTTAGGAGATGAAAAACACAAA
WI-14408	60	T A G	GCAGACACAC	TTAATTGTGTA	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAATGCAGACACACTATTACAGGCTG[T/A]AAAGTAACAATGAGTTTTACACAATTAATAATTAACACATACCTTATGGGATTTGTTGAATGA
WI-13683	47	C G ---	---	---	TTTTGTGTTAAGAACAGCATTTTGAAAAATAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAATTTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C T CGTCT	CACCATGGCA	CATTGAGATAA	TTAGAAAACGTATAAAGCAACACAACCTTTTGGGAAAGACCATTGGCAGCTCCTTTGTGCTA[C/T]GTGATAAGTGTGCTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---	---	---	ACATGGCAGATACAGAGCTGTC[G/A]JCTTTGAAGACCACCACCTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAGCGTTGAAGGGTGACCAAGCACATTTGCACATGCAAAA

WI-16002	59	T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTCATTC/GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGCT
WI-15361b	101	A G A	CCCACITGAAC TCAAAGTCATC	AAACTAAAG CTTTGTGCCTA AAA	GTGGAAATTTTAAAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAAGTCAAGTCAATCA/GJTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAAACCA
WI-14759	73	T C	GCCTTTGACTT GTGGGG	TCCACACTGC OCCC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTTGGTTTTATCAAACTCCTAGCGTTTGACTT GTGCGGTTC/GTACTCAATGGGGGCGAGTGTGGACGGGAGGATTGCAACCAAGATTTCATACTG CAA
WI-12535	50	A T	CTAGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTATTTCAGGTGGTGAAGGAGGTTGAGGTGTAGATAT/TJCTTCTCTCTTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCC
WI-13805a	112	G A	AAAGGCACAC GGGAA	CTCAGCCTGCC TTGACC	TTCCATTTCATTATGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTGAGAAAAAGGCACACGGGGA/GJGGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T C	---	---	ACACAATATAATTCCTATTC/GJGAGTGATTAAACCTTATTTGTTTGAACCAACAAAACTAC AAGAAAAACATTTTCAAAACCTTTTTTTTCAGGCTGA
WI-14808	52	T A	ACCCACACA CTACCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAACACCTTTAAGCAACAGTTAAAAAGTACCCACCACACTACCCTGTT/AJAAAACTTTAAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAAAACACAACTGAAGCCCCCATGTA
WI-14816	29	A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTATT/TJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGATATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-12542c	71	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/GTJTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT/GTJTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAAAACTGGGGATACAGCAGTAAAGAATACAAAAATCCTGCTCTCTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C	---	---	TCCTTGGAGGGATAGAGGACAGAGTGTT/CJGTTGATTTTCGTTTCAGTTTGGTTGTCATT GGTTTTGTTTTTGTCTAATTTTCCCCACCCTATAAAAAGCAGTGCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACAG GAAAATACCTT	TTTGTTCCTA CTTTTACAAA CTTT	ACATTTCTTATGATAGCAACAACATAATATGATGGTGTACACGGGAAAATACTTAAT/A/TJAA AGTTTGTAAAAGTAGCAAAACAAAATTGGAGTATATACTATAAGTGTAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A	---	---	ATGGCAATTTACTTTATAGCAATGAACAAAATATTTGTCAAAGGGCAAAATATTTTGTCTG/GA/JAG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	GACATTC GGCTCTCTAAC	TGGGCTGCAG ACACTC	TTTTAATTAACGTAAAAAGGACGACATTCCAAGGCTCTCTAACA/T/CJGAGTGTCTGCAGCCCCA TTCGCTTGGAGATGTAATGTTAACCCAGGTGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTCAG GCCATTATT	ACGGAGTCGTCTGTATGTTCTTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAATT AGAAAAATCCAAATTGACAGATATTTCTGCA/GA/JAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C	---	---	TTTTGTACCTATTCCCTGTTTTACGTGCATGTACAGGAAGAGTTGTCTCATAT/CJAGGTGCCACTAAGGAAA ACTTCTCCAT/CJAAAGCTGCCTGTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGCATCT GCCTGTGTTCTGTCTT
WI-14898a	50 A C A	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCCT AGTGGCACCT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/CJAGGTGCCACTAAGG AAAACCTTCTCCATAAAGCTGCCTGTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGCATC TGCCTGTGTTCTGTCTT
WI-14907	48 G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGGCACACATTGGACTCTGAQ/GA/JATTCCTCTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCCATCAATCAGTACTCTCTGCATGCAGAGGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTCGGT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAAGCTCAGTGCACCAATACATTCACTTCTGTGTG/GA/JAAGGTCCTTTTC CTGGTTTGCAGACAGATACCTTGTGTATCCTCAGATGGCAGAGAAAGAGGAAGTAATCT
WI-14913	88 C A	---	---	CTGATGCTTTGACATCTGGGGCATTTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGCCAATTTTC TAGTGATAGTAGAGGACTCA/C/AJCCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCAAACCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCACGGA CAATAAATTC	ATTTCTTGATTGGCTGTGTAAGCCCTGTGAAGTCATGCACATCTGGACACAGTTTTTCTCTAGCA/G CJGAATTTATTGTCTGGGCTTGATGGCTTTCACAG
WI-14926	49 T C	---	---	GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCATTAGCGAAT/CJACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTTCAAAATAAAAATTTTCCTTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAAACATATC AAGGAT	TGGAAGAGATT OCAGGOC	GCATCTTTATTACCACAGAACTCATTTATGTCCTTAATCATTGTTTAAATATAATATAAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCCTTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTGTGGTATTGGGGAGCACGAGGGAGAGCAA
WI-14946	47 T C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCACAGACATAACAAT[C/T]CTCTAAATCATCCTCTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATACACACAGTACTTTATGGAAAGGATT
WI-15987b	80 A G	---	---	ACATTAAACAGCACAAATTAAGGGTCCCAAGAGGTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCCGGTCCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAAATTAA GGGTCCAA	GGAAGGCATA CCAACCTC	ACATTAAACAGCACAAATTAAGGGGTCCCA[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCTCTTAAACCTCTCAGC
WI-14948	56 T C G	AGGAAACTG CTAATTGTCA T C G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTCTTATTGCCGTCTCTCAGGGAACAGGGAACCTGCTAACTTGTCAAGT[C/T]TCCAACA ACTGATGTAAGATCATCTCTGACCATAGCAACCTGTAAAGGCTTGTCTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTTCTACAC T TGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATCTCTGTTATCAACTCTCTGAAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCAATTCAT TTGGGTTTTT	GTGATTGATCTGTAATTTATGGGATTATTTCAACTCTAAAATTCACAGATGAAAATAATTTATCT CTTTCTTTTCAAGGG[A/G]AAAAACCCCAATGAATGCATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAAATTCAAAGGA
WI-14976	35 C T	GTTGATTGCT TCGTTCAAAG T	TCAAACTAAAT CTTCCATTCTA AGC	TATTTTTTAAATGGTGAATTTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGCATAGTGGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTTAAATCATGCTACCAGCCCATCTAAGCCAAATTTCAAACACCACCTCTGCATT AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCAACTGATCGGAAAGAAACGTA
WI-15002	72 T A	---	---	AAATCTCTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACTGAAATGCTTCTTGA TTTCC[T/A]TTTCAAGTTTAGGCTCAAAATGGGCTCTCCTCAAGGCTGGACCTCAAGGCCAGTT
WI-15000	90 G A	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAACTT CA	TCAAGCCCAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTTTATACACAATACCTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCACAAACAGAGGACTCACACCTGTGTCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTACAGCTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CCTGCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCCTTATATTGGAATTTCTA[C/A]JAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGTACTTTGTGAATGCTTCCAAAGTACAAATCA[T/A]CTCACAAATACCATATACAACATACT TTCAATCACAACTCAATATAAAATAACCTACAAAATCACATTGC
WI-13712	40	A C T C A T T G	TTTACTTTGTT GTCAATTTTAT TCTATTG	CCATAAGGCTT CACACTTTTCT TAT	TGGGATACCCCTTTTACTTTGTTGTCAATTTTATTCTATTG[A/C]ATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTGTTTAAATTTATGCAAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA[C/T]ATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAAGTTTAAAGAGGACTATTCTTTAAACAAAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGCAATTTGAGTGTCTTATTATATTGGGAATTGCAGTGATTAACATTTGTACAAAT GCACAAATCTTGCTCTCTCTC[T/A]TGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGICCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA	TGCTGTGGTG AATAAGATG	CGGATATAATTATGTACCCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT[C]CATCTT ATTACACGAGCAGCACACCCACGACAGTAGAACAGTCCACACCTGATAAAATTGCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAAATAA[G/A]AATCTGCAAGTTTCCCAAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATTTCCAGTATCATGTAC GCACTAAAAAAAT[C]GTGTGCTTGCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A T C G C	TGAAGATTAA CCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGTTATTTGTGTATCCCAACAGTATACAGAAATCTCTATAAACCAACCCCAACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC[A/C]TCTCTTCAAAATGCACACAAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA ATGT	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATAATAATACAGCTTTTTTTCATTGAAGCTTTGTTACCTT TACTATCTAGGCTATTGGAGTGTCCCCCAG

WI-15100	74	G A	...				TCATTACAGCCAGAAATAACCCAAATATTCCAAATAAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCCTCAAGACAAGATGGACAGCGAGCTGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T	AATTACT			GTACCATGTT ATATTTCTTT TAAGAC	TGGTACAGAAATGTTAATTACAGAGGGCAGTGATTCAGTTAAATAAATAAATAAACCCTTTATTTT CCCAAAATATAAAATTAATAATTAA[A/T]GTCTTAAAGAAAAATATAACATGGTGACAGCTTT TCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[G/C]GCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002c	89	T C	TCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A	TCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCACATGGAGACAGAAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G	GGACACAA			TGGTTTTGGG TGTTTTCTT	TCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCACATGGAGACAGAAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-15116	96	C T	GTTGCAGTAA			CCTGAATATGC AATTATTTAT ATGACA	TTTTCAATTTATTTCCAGAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTCTATAATAATAAATTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37	C T	AATGGGAA			TCAAGCGACCA CCAACAC	GCAAAAGCAAAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTGGTGGCTTGATACCTGGT GCTTGTGTGATGGAGCAGAAAGTCTTCTGGTCCATGCAGGGGCGTCACATATTTAACTGCACATAAT TTGGGCAAACTGTCTATC
WI-15153	40	A G	GCATTGCA			AACCTCAGATA AGTGCAGTGTCT T	ATTTACAGTTGGCCAAAGATCTCCCTTATGTGGCATTGCA[G/A]GAGACACTGCACCTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCCTAA
WI-15215	84	G C	TCAATGGG			CCAACAGGGGA AAAGTCA	CCTTTGTCTCTGAACCTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTGAGGTATGGC TTTAGAATCAATGGG[G/C]TGACITTTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C T	AGAAAGCAAA			TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGTGAAGCAAGCGCATTCATTGGATGAATGATTATGTGTCCAGGACCTTGAGGAC CTAGAAAGCAAAAC[C/T]GGAGTGATTATGCCAATCAAAATTCGAAGTTGGAGATATGCTAAAA AATTTGCTAGTGCAAAATGGACCCAGAAATGGAAAGGCTATGTAACTACACAG[G/A]TATGCACACAC AGCCATGTCAAGTGTACAGATCCTCTTGTGCAATTCAGCTTTCTTAAAAACACATCAAAAGGCTGCA
WI-15152	51	G A	
WI-15123	55	C T	TAGGATG			TGCTTAAGGG CAACAGAC	TGACTGTATACCAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTAAGCAATTTACAACCTACCTGCGGGAAGAAACAGACATGCAAAACACGAGATAAAACACAAT

WI-15182	49 C A	GCACAACCG	GCATGGGTTAA	GAGACTGCCCTGTGACACAACCTAGCTAGCTGCACAACACAGGGCAAAATAC/AJTGCTGGATTAAACCC
WI-15198	38 T C	GGGCTTGGC	ACCTATCCGTC	ATGCTAATGGGTTACCTTTATTATTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-12601	42 T C	ACTATG	AGGCAGAGTAG	GTGGACCTTACAAGTACCATGGGCCCTTGGCACTATG/CJCTACTCTGCCTGACGGATAAGTTGGC
		CATTATTGAG	GTTGTAGTCTT	ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
		TATCTTGGCTT	ACATGCTTACG	TCAAGTGGTAATAGCCATTATTAGAGTATCTTGCTTTGAT/CJGCTACGTAAGCATGTAAGACT
		TGAT	TAGAC	ACAACATTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACATTTTGTGTCATTCAGAT
WI-14510	104 A T	TGGAAAATA	TTGAAAATGGT	T
		TGCATAACAA	TAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTTAGTGAAGTACACCCAGATATTTTGGGGAGAAGAG
		CAATTGCAAT	GGACCTTATCT	TTGTTTGCTTTTGTGGCAAAATATGCATAACAAAAT/ATJTGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57 T C	AAACACCATC	GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAGATTGTGCATTTGCAATAAACACCATCAT/CJCTGAG
		CA	GGACAAATTGT	TCCACAGATAAGTCCCGGAGAGGGGCTTCCCTCTCTCGCTGGGTGACGTTCCCGAGCGAGT
		GCATCATATG	AAACATAGCT	GAAGCCTTTTCTGGAATG
WI-12634	52 T C	AAGT	AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAAGTGTCTAGCAGTATTAT/CJGCTATTAGCTA
		GGGCTTGACAC	GGAAAGCCAG	TGTTTACAATTTGCTCGAAGGGGTCTAGATGTGTACACCCAGAAAGTGGTGTCTCTGA
WI-15249	34 T C	AAAGTTCTAA	AGATTTTAAAC	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTT/CJTTGTTAAAAATCTCTGGCTTCTCTGGCTGG
		AAAGTCTAA	AA	TGAGGAGGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGCCCGCATCTGTTCCTCCACTCCCCAG
WI-12159	28 C T	GCAATGC	CCCTCTCCTCA	CCACATCTTGGCTCT
		AGTGGATGC	GTGCATTT	CTGTCCGGGAAGACACCGTGCAAATGC/CJ/AAAGTGCCTGAGGAGGGGGGCTGTGTGACTC
		CCTAGTGGCAT	TTGCTACTAAA	CCAAACCTCGAATATTTTATGAATCTAAGAGTCCAGACGCGAGTTCATCCACGGAGATCTGC
WI-12648	41 A G	TAAGGATGC	AGTGGACATCC	TCCCAGATTGTATGGAATGCCCTAGTGGCATTAGGATGC/AGGTAGGATGTCCACTTTTAGTAGC
WI-12684	64 T	ACAGCTGTGC	T	AACCGATGTTAATTCACACTCTCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAACCCACA
		AAAGGATGAA	GGAACAACAA	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAAATATTAGTAACCATGTCTGTAAACAGCTGTGC/G/
		GCTAATCATG	AGCCTAAATGG	TJCCATTAGGCTTTGTTGTTCCATTAGAGAGCACAGGAGAGGAAATTTAGCATAAATCTT
WI-15260	75 G A	GA	TCCTCCAGG	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCT
		CATGTGGCTGG	AGCTTGC	AATCATGGA/G/AGCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGAAATTA
WI-15325	39 T C	GAGGC	CCCTCCACCAT	TCCTG
		AGTTGGCATTC	GATTGTGA	AAGGTTTAAATGGACTCACAGTTCATGTGGCTGGAGGCT/CJTCACAATCATGTGTGGAGGCAAAA
		AATAGCCTAT	TGAAACTCCCA	GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123 C T	C	CATGGAGTT	TATTTGAGTATTCATCCATGGGCTTCTCACTCCCTTATACATCTCCAGGGTTGAGGTAGTCTACCC
				CCATAGGTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATG/CJ/AACTCCATGT
				GGGAGTTTCAATAA

WI-14528	62	T G	TTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAAATTT/GJTT GAATTATAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCA AGTCTTTG	TATTTCTTGGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAGGAAAAAGA ACAAATTT/C/TCAAAGACTTGGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA/C/AJCTGCACGTGCACCTTTTCATATACAGATCA
WI-15353	37	G A	---	---	TTTATGGCTGTCTCTGTAATACAATGTGGTGAAAAAC/G/AJCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGACTGCAAGACCAGTGCAGGCACATAGGCTGATTAAATCAGTGG
WI-14580	100	G A	CATTCCATCT GTCITGCA	CCGACCAAGAT CCCTOC	AGAAATTTTCTTTTTTAAAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAAATAC CTAGTTATTATACACATTTCCCATCTGTCTTGCA/G/AJGGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T C	GGCTGCATTT GGCTTA	GCCCTTCTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACACAGAAAAAACACAGACTACACACAGGCCCTGCATT TGGCTTAT/CJGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGAAATGTCT
WI-8039b	97	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTCAGTTAAATATGTAT/CJGTGCTCGTGCATGTATGATTAAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGGACACACCATGCAGAAAAAGACAGGGA GACCAGACACTCTGGTTGAGATGATTTTAAATGCCCGCAGCCGACACCCACA
WI-8039a	87	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTCAGTT/CJAAATATGTATGTGCTCGTGCATGTATGATTAAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGGACACACCATGCAGAAAAAGACAGGGA GACCAGACACTCTGGTTGAGATGATTTTAAATGCCCGCAGCCGACACCCACA
WI-8044	107	C A	---	---	CACAACTTCAGAAAGTTTCTGCAATTTGCTCTCTCTGATGCTTAAAGATTTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCACTTCAAGGTTTCTCC/CJAJAGTATGGATTCTCTGATGATTAAATA AGCCCGAATCTGGCTAAAGGCTTCCACACTCAAGACATTTGTAAGGTTTTTCTCCAGTGTGGAG TCTCTGGTGTGCAAGAATGGAACCTCGGCTGAATGCTTTCCACACT
WI-8550	32	G A	GGGAACATCA ATGCAACAAG T	TTTGGGCTTG AGTTTACAAAT	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AJAAATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T A	---	---	TATTAGATAAAACCCCTTGTCCCGATTTCAGGATGTTTAAATTTGCTCTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAGT/AJGATGGACAGCAGCAGAGAGGTGGGGTCTGAAAAATGTAAATCTTT GTGTCGAAGGCACCTCTGTGGCTTCAAACTGCCCTCTGACAGGGGATGCTGCCCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG

WI-6192	91 A G	GACTGCTAAG GATTTAATTTG TAAAA	TGAAGTGTAG ATGGCTAAGTA TAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATAATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAATTTGGAT/GJATTTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105 T A	CACATGGCAA TGATAATAAA GAAA	TCTATCCTCAG AGGTAGTCTG CA	AAGTGATGTGCTCTACAATACATTTCTCAAACCTCAAACATCATGCTTGAAATATACACTGAACCTT GTCACCAAAGAAAGTCACATGGCAATGATAATAAGAAAT/JATGACAGACTACACTCTGAGGATAG AGCTCTAAAGAGATAAAACAATGGAATTTGGAAAAAATAGGAGTAAA
WI-6213	164 C T	---	---	CATATGCTGCTTTATTTCTGTAAGGATACACTGAACGTTAGATGATAATAGCTAATGACAGAAATGT AGAAATGAGGCATCAGCTTCTTAACCACTCCTACAAGAAATGTTAGTATGTATTGCTATTACATGTTT ACTTTGATATTGCTCATTAATACTATGTCT/JATATAATAATGTAGAATACAGTAAGTAGGTGATCC TGCATTCAGGTAAGCGGTAGGTGGAAATCCAGATTCTCTTGAGGAAAA
WI-6217	131 C T	---	---	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGGTGGGCTGTCTATCTGTGGTG TCAGTCTTCTGGCCCTGGCTGTGAGTGCTGCTCCAGGGCTTGACAAGCAGCTCATTTCAAG[C/T] GGCCACCATGGCCCTAGGGTCTGTCACAAGTCCAGAGCAATCATGGCTTCTCGTATATCTGATCC AC
WI-6238	175 G A	---	---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACCTCTGGTTTGTATTTATGCTTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTTGGTATTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAAGTTCTCAAAATTTG/JGTTCCAGACTTCAGGAAAAATGATT TCCACATGGTAAGGCCAGAGTCTCAGTGTGGTCATCCAGAACGCTTG
WI-6272	86 C T	GCATTTATTCA GGGAAAACCT TAA	CTGTTTTTGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGTCATAGGGGATTAGTCACTGTACAGTCATAATAATGCAATTA TTCAGGGAAAACTTTAATTC/JTTCTTTGTCTCTCCAAAAACAGCTGCTGGAACACCTCAAATTA GGGATGTTTCTATCTAAAACACCTTTACTGAACTTGATTCCTTTGGCCAGAGGAGGCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTGGGCAATAAATGAATACTTGATGCATTTACAGGCAAGAA TCCCAGCATCCCAGAGAAGCTCTGTGCTG/JGCTGAAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAGTTCTAGTCTCGCCTCTCGATTTTCCCTGCCAGCAGTCTTCTCTCTCTCTCTGCCCC TCIG
WI-6303	96 G A	CCCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	ATGCTTTTGCATGATTCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCCAGCGTGCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTAGTCTCTCTCTGCTT CTTCCCTTACATTTCTTTGGGGA
WI-6315b	193 C T	---	---	ATGCTTTTGCATGATTCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCCAGCGTGCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGT/CJAGTGTCTCTGTT CTTCCCTTACATTTCTTTGGGGA
WI-6315	187 T C	---	---	CTTCCCTTACATTTCTTTGGGGA

WI-6375	28 A G A A	GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAGIAGIATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTTGTTCTGATAAGACAATTCAAACATACAAATCAAT TACAACAAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAAI/A/GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTTGTTCTGATAAGACAATTCAAACATACAAATCAAT TACAACIATATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATAATCTCTGGGCACATGGATCCAGAGAGATTTGCAGCAGATTTTCAATATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG(G/T)ATCAACCTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGGAGCTCCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACGCAACAGCTAAAACTCTGAGAGAAAAC(C/G)CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAAATTTACATGGGCCCTATTTATTAAGGACATTTGTAATGTTTCCACTTTGTTTAA IC/T)AATTACAAACATGGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAAATTTACATGGGCCCTATTTATTAAGGACATTTGTAATGTTTCCACTTTGTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558a	42 G C ---		---	AACCAACAAACTAAGAAATGGGAAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGATAAA AGTTGTCAAT/CJAGCAATGGATGCTGTGTCAGAACATACGCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAC
WI-6629	75 T C G C A T A	TCITTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAAATCAATCAATCAAACTCCAGCTGTTTCTTCTTCTTT TTACTTAGCAAGGAAACCTTTAGTGAATGCTACTTGACAAAGAAAGATCTTCTCAAGCACA T/CJACCCAACTTGAAGGTGATTGAACCCCAAAATAATGGGTGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAACACCCACCATTTATTAAGGAGAGTACTAGGAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGCACAGACTCTGGAGCCACAGC(C/T)GGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAAGCGGTATCTGG
WI-6690b	106 C T A G C C A C A G C	CAGACTCTGG	ACATAAAATA TTGCAGTGAT TAGCC	

WI-6890a	28 T C AGAG	AAACACCACG ATTATTAAGG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACCATTAATTAGGAGAGT/CJACTAGGAAAACTACCAACACAGCATGTGAAC AGTTGGCACGGTGTAAAGGACACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTTA TGTTAGCAATTATAGCTGGTCTGTGTATACCAAGAGCGGTATCTGG
WI-6770	53 A G AACATCACA	CAAAACCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCAAAGTAATCCAAACCCCAAAACATCACA/A/GJAATTATTCAT ACTATTATACACTCCAAAGCAAAATACITCAACTGCAATCC
WI-6686	151 A G A	GCAITCTTCCA AAAACAAAGA	CCTGTAAAGT ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTGAGCAATCAGTAGCAGTAACTCTTGACCAAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTTACATTTAAACATGGTAACCTCAAGCATTTCT TCCAAACAAAGAAAT/A/GJACATTTGGAATAGTCACTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGATGG/C/AJCTTCTTCTCCAGCTTTTGTGAACAAAC AATTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTCAGGTACAAGGCTC
WI-6844	225 T C	TAAACTGTCGCACTAGCATTACGTCCTCTTGACATTAATAAAACAAAGGATTTTCTCTCTTG GTATTTCAAATGATGCATTATACAATAACGAAAGTTAGAAGTTAAATGCAACCTGATTAATATG TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTCTCTTCTTATAAAATGGAAATTTAA TATTTCTCTGATAGTCTGAGGTT/CJATCATTATGAGTAGTGCAAGGTG
WI-6824	112 A G	CGGTTTGTCTACACTTAATGGTTTTTTTTAAGGATTTTTTTCAGGCTTGTGACGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGTCACAGGTGCTGCCAA/A/GJACCTTAGAAAAATTACAT GACACGAGAGAAATGCGCTCTTGTCTTGAAGAGTACAGTACGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C AATC	GAAAAATGAG ATGCAGTTAA	TCACTTTGGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCCAACATGGAAGTGTCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC/CJAGAATAATTAAGGCCACAAAGTGAACCTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C	TCCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAATATCTGATGAACCTTGATGAACGAA AAGAGGTCTCTTAACAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCAGAAAACTTTGCCCTCCCAAGGAATGTTTTCTAATTTGGTTTCAAAGCACACTGGTTCC CACTTTTACCACCTTT/CJATGACATTGGACAAATAGTACTACTCTTTCTAC
WI-9413	112 G C	GCCAGTCTCTAGTAAGTCTTAGGGACATGACCAGACCCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATCTAGTGGTGGAGGATACCGCTGCTATTTCCAGAT/GJJAAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T	AAAAGCTTTAAAAAAGTGGTGTCTCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCAGCT ACAGCCT/CJGGTGCATCTTAACCCCTCTCTTT

WI-9617	37 G T ---			TGCTCTTTTATTACGTTTCACAACACACGCCGTG[G/T]GGCAGAGTACCAAAAGTGCCCGCAG CGCCACGCTTGGCGGGAAGGCTCTATTCTGTCTCTATGGAGTGAATTTGGGATGGCCAG CTCCAGAATGTTCCAGTGGGGGACCTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCAACCA AAGAGTTGCACGATGCAGCTTGCAGTGGGTCCAGCGCGGTGCTGTG
WI-9657	121 T G ---			AATGCTGGAGAAAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCACAAATAAAGT[G/J]ATAATCTT TGATTAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114 G C GCTGGGA		CTCCCAAGTA CAGGTGTGGTG T	CAGGTCCTTGCTCTGCCAGGCTAGAGTGAGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATG[G/C]JACACCACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTC[CAAAAAACAAACCAACTAAC CAGGGCTTGCTCTGCTGCCAGGCTAGAGTGAGGTGACACAATCAAGACT[C/G]JACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTC[CAAAAAACAAACCAACTAA C
WI-13119a	51 C G ---		---	ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71 C T AGCTTTT		TTAGAAATTTT GTGTATTATAT GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[G/J]AACAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTGAGAAATATGAATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-12988	36 C A CTCAGTACAA		CAAAGTGACAA CTACTGATGCT GTTT	TGCTATTTCATGACAGACACGTCAGACAAAATATCTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAAACCCTGAGACTTT[G/J]ATCTGCAAGGGGTTTAAATAAT GCAATATCACATATATTTCCATTTTAAACACCATATTTAAGTTTCCATTTTCTTAAATAGAAAAATGA TAAAAATGTTTCCCCCAATAT
WI-13020a	108 G A CTTT		CATTATTAAAC CCCTTGCAGA	TGTATAAAAAATCCAACTGTTCCCAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[G/J]TACAAAAAACAGCATTTCCCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTGTGTTT
WI-12837	87 A G AAAGTCCA		GCCATAGGAA ATGCTGTTTTT	AGTGTGTTT

L42611b	50	G C	---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCTGTCTGCTCTCTCTGGCCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCCTCACCTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
L42611	34	T C	---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTTCTCAGGTTGCCTGTCTCTCTGGCCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCCTCACCTTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179	C T A		TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCAACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAAACATGTTGT
WI-1172a	17	C A	---		---		TGAACGTTGGTTAAAC/C/ATAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAAACATGTTGT
WI-1177	35	G C A		GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAAGTGTGAAAAAATGAAAGAA/G/C/JAAGAAAAAAGAGTCTAAATATTCAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCCACTTAATCTGCAATTTTGAAAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCAATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTAAACATGG CCTGGTG
WI-1231b	141	G A	---		---		TCCATGGTTGGTTGCTACTGACTTTTGTAGCCCTACTGCCCACTATGCATTGGAAACATCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAAACATAGGCTCTTTATTTCTCTCTTTTCAATTTTCTT TCAC/G/ATTTATCCCTCACCCCTGAACGCCCTTCTCTCTCGTAGTGACATTTTAAAAATCCACTTTAC ACATTCGGACC
WI-1231a	126	T C A		GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTGGTTGCTACTGACTTTTGTAGCCCTACTGCCCACTATGCATTGGAAACATCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAAACATAGGCTCTTTATTTCTCTCTTTTCAATTTT CTTTCACGTTATTCCTCACCCTGAACGCCCTTCTCTCTCGTAGTGACATTTTAAAAATCCACTTTACA CATTCGGACC
WI-472	114	G C A C A G A A A A G		ACATACATAT CCATTATACA	GACCTTCTTT TCCAGGCC		GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAAACAGAAAAAG/G/C/JGGGCTGAAAAAGAAAG GTCAAGTGAGATTTCAGATATTTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG T TACTCTATTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGTGTTACTCTATTTTGTTCCTAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAACTCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT	CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTTTCATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTGGTATAATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112 T A	TCACTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAAATAAGATGG TAGTGAGCGAACAGAGAGGTTTCATTGACTCCTAACTGAGTACTTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	TCACTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAAATAAGATGG TAGTGAGTC/TTGAACAGAGAGGTTTCATTGACTCCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAACAGACACCCCTGGCTCTTCTCACCAGTCCACATGGGTGCCAAACAATCCCACATTCTCT ACATCTCCCCACTGGCTGCCTCTTCAACACCTCACCA/AGTCTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGATTATCAACCTAGCC/AGTCTGTCATGTGGGATTAGAATAAAATA AACACAAAATGAAAACACACAGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACCGTAAAGAT AATAACTTCAA
WI-991	37 A T	TGCATTATTATGCACCAATAATAACTTCTGTACAT/ATTCATTATTGTATTTCATTATCACAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGATTCCGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70 G C	CAGTATCTGA AGTTTTGTCT OCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGACGTGGATAGTGTTTTGAAGGCTCTGCTCAGTATCTGAAGTTTTTGTCTCC A/GC/JAGAAGTCAATTTGTAGGTGTTCTGGCGTTTTTGTCTACGTTTCCATTTCTCTAATACACTGC CGTCTAAGGGAGGGCTTGCAGACATTTATCAGATGGCTGTTTGTCTGCAITCTGTGCACTGAAG
WI-5381	178 A T	TTTCATGCAGAAAGGTCCATGAGTTTACAGAAATCTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTTGCTCATGAAAATTGGACAGCATGTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAATCATACTCTATCCACGTGCAGAAACTGGCAATAGTTTGTG/ATTTACTAAAACACAAAATGT TTAATCTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5791b	76 G A	CTATGTATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCTTA GAACCTCAG/G/ATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCCAAGGTA AAAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCTGTTTGT TAGGAA

WI-5791a	44	C G ---				CTATGTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTC/GJACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTTGCACCCCTGTTTGT TAGGAA
WI-5406c	120	C T ---				CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/J]TATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAGAAAGAGAGAGGCAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGCTCAT		CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/J]TATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAGAAAGAGAGAGGCAA GG
WI-5406a	42	A G ---				CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAG/GJGCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAGAAAGAGAGAGGCAA GG
WI-5798	48	G C TG	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTT TCAAT		CCATTCCTCTTCCCTCCCTTATCTCCCTTGTCTTTTG[C/J]ATTGAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGATGCTATATATGGGTATCA
WI-5415	54	T A TTT	TCTTCATGAAT TCATCTTTTCAG	GGACTAATTCA TGATCCGATCT		CCTGCTAATAATAATTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[J/A]TAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG		TGTTTTAACCCAGGACACCTCCACAGAGAAAATCCAAGAG[C/J]CTTAAACCATATTTTGTGTTTA GAACTCCTGTGCGCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A G CTGCAGTCG	TGTCATTTATG CTGAGTCG	TTACTTCCAGG CTCCAAGTATT		AAGCCAAATTCACATTAGTTGATGAATTTG/AJAATTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG[A/G]A ATACTGGAGCCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29	G A AATTT	CCAATTTTCAG ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTG/AJAATTTACAGTATCTAATGCATGGGCATCTGTTTCAAC AACTCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTGGAGCCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38	T C ---				TCATGAGTCTTTCTTCAAGAGTCTGTTGTTAAAGTCCCAAT[C/J]CAAGAAAGGATCCCATGGCCTAAT GAAAGATGATACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C ---				TAATTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTTCATGCTTACATTTATTTTTTT TTTCACCTAGTTAAATGCTTTTCCCTTGATCGAATGGCCAGTTTATACATATCTTTAGTTC TTTCAAATTAATGCCACCATAGAAATAATTTCTAACCAACCGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCAATTACTCTTTACAC
WI-5546	40	C T A				CCTTATAACCCCAATACATTTTTCAGGTGAAAAAAGGGAAAA[C/T]ACCCATGTTTTCGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAAATTACAAATGCTTGAGTGTAAATCTGATGTGGGAAATAT TAGAAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T				TGTTGTCTGCACCTCCCCAACAGTGGTCAATGAGCCTCAAGGGTTTGTATTGAGCGGGTATGGGT GGGGCTATCGGCACCAAGCCTTTTATAGATTC/TCTTGGGCAATTTGTGCACCTAGTGTACAG TAAGTTGATTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGGTGGATAGACATGAATAACTCTGATGATACTGGTTGTATCCCTGAA TCCTGCAATATACACATGATTCATGATGATTC/TCCATTTTGAAAAATTAAGCTTTTGAATTTGTTTCCA ATG
WI-5836b	161	C T ---				TCGGGTATTAGGATCGGTTCAACCTCGATGATGATGGCGTTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACTGTTTCATCAGAACACTTCAACAGCG
WI-5573	58	C T				CAGGACCTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTCTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATGACACGGCTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCTGA TTTTGCCATTTCCGTATATCAACAGAGAGCAGAGGGTGG
WI-5850b	134	G A ---				CAGGACCTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTCTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATGCA[C/T]GCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCTG TTTTGCCATTTCTGTATATCAACAGAGAGCAGAGGGTGG
WI-5850a	92	C T ---				TGCTGTATTGACACATAGTTATCTGACAGTAAATCATTTCAACATCACAATATCTTATTCTGCCTG TCACACTAAATTTGCAAAGCATTCATTTGACTATTAAATGAGCATCGTGTCAATTC[C/T]CAGTGT TTAGTTTCTCAAGAGAAATTATGCTGTTCTCTGTAACCTCAAGTA
WI-5612b	125	A T				TGCTGTATTGACACATAGTTATCTGACAGTAAATCATTTCAACATTCACAATATCTTATTCTTCG CTGTACACTAAATTTGCAAAGCATTCATTTGACTATTAAATGAGCATCGTGTCAATTC[C/T]CAGTGT TTAGTTTCTCAAGAGAAATTATGCTGTTCTCTGTAACCTCAAGTA
WI-5612a	44	T A ---				TTAGTTTCTCAAGAGAAATTATGCTGTTCTCTGTAACCTCAAGTA
WI-5636	26	A C				TGAGAGCCAAATTTTATCCGCAATAAA[C/T]TCCCAAAGTCTCGATGGAGGCAATTCAGAATCGGG GCAGGGGAGGCAGAAAGGTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ---			---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAAATTAAAC/G/AAATATTAATATTTTATTACAGAGGAA CTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTCA GAGAAGACAGACAACTAAATAATTCACGG
WI-5865b	99 T A ---			---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAAATTAAACAAATATTAATATTTTATTACAGAGGAA CTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTCA GAGAAGACAGACAACTAAATAATTCACGG
WI-5865	165 T A ---			---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAAATTAAACAAATATTAATATTTTATTACAGAGGAACTC AGAAAGCCAGAAAAAATGACCAAGACACAGTAA/JCCAGTCTCCATCTTCAAAAGGTCACAGTCTTC AGAGAAGACAGACAACTAAATAATTCACGG
WI-5874	76 T G	CATAGCATGG ATAATATTAT ACAGAAAAA		CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGATTTTCATAGCATGGATAATATACAGAA AAAAAATTT/GTACATATCAAAATGACTGAAACTTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTTCAGCCTCTCAGTTTTTCCATG/A/TTTTTTTCATAATTTACTCTCTTTCTGTC ACAATGTTCTGCTTCGTTCTGATTTCACCTCTCATTTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAATAAGTAAATG
WI-5752	36 A T	CAGCCTCTCAG TTTTTCCATC		GACAGAAAAAG AGAGTAAATT ATGAAAAA	TTAGCAGAAACAAACAAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAAATAC/GJC CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAAGCCGAGTTTTCGATTTCACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA CATTGTTGAAACGAAAGCCACGTTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760b	61 C G ---			---	TTAGCAGAAACAAACAAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAAGCCGAGTTTTCGATTTCACACAGTT GTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG/G/ATCCCAACGAA ACATTGTTGAAACGAAAGCCACGTTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760	187 G A ---			---	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG/AGTTGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGTGTAAAGACTACTCAATTTCTCAGTCTTCTTGCTG
WI-5944	52 A G	TTCTCACCATG GGAATCTTG		GGGTGGGATCT AACTTGCA	GAGTTTAAATGAATCTGTTCCCTCCTAAAAACCTCTGTTCCCCCACTTCACATTCAGCAGATATT CTTTCAATGGGTTATTTTGGCCAAAGTCATGAGGAGATGATGTAATTTGATGATCATTTCAAGAGTGTGAG TAATGCTTGGTA/C/TJTTGCTCTGTGCGGTATCTGCTCCAATCAOCCATTCACCTTTATTTCTCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148 C T ---			---	

WI-5967	165 C T ...				GAGTTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCAACTTCCCTCAGTTCACATTCAGCAGATATT CTTTCAATGGGTTATTTGCCAAGTCATGAGGAGATGCAATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATTC/TTTGGCTCCAATCACCCATCCACATTTATTCCTATTAT GCTGAATGAACGCTTATATTACAG
WI-6093	53 G C ...				GGTAAGATCCAGAGCCACAGGTGAACCTGCCGTTATTGAAGTCTTTGGCCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCAGTGGCCCATTTGAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAACTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA			GACTCTGTCTCAAGAAAAAATAATGAATAATTAAGCACTTCTTAATTAAGCAT CTACAAGGTACTTAT/CJCACTGTTCTGGGTTTCAATCCTCTTCACTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAATTTGCTTTT CTC
WI-6450	45 T G TGTACA	CCAATGACTT ATTCTATATCT			ATAGGACAGTTTTCTTCCAATGACTTATCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAAAGGCGAGGCTATGCCAGGGTGGATTATTTACGGTCAATGTAATATGCATGTAAGACTA TTTTACTGGCTTCTTTATGCTATAAACAAAGGTATTGGTCTATTCAACAAACATGTGTCAATACAG
WI-6461	88 C T ...				CAGTTGTCATGTCCCTCTGGTACTAGATATAGTCTTTATAGAAATATGTGGTTTGAATAAGGCCACA AATTATCTATAAACACAC/CJJAAGGAACGAGGCTCAAAAGTGAACAAACCGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAATAATAATCCGTGACCTCTTA
WI-7466c	141 G A TTGTCCCTGG	TTTTCACAGTC			GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTCTTTGGTCCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CJATTCACTGAAGTATGTAATCAATAAAGACATGCAAAACCTTTTACAGTCTT CCTGG/GJA/AAATATCTCACAAAATTAATTAATAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA			GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTCTTTGGTCCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CJATTCACTGAAGTATGTAATCAATAAAGACATGCAAAACCTTTTACAGTCTT TGCTCTGGGAATATCTCACAAAATTAATTAATAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTTT
WI-9814	104 C A ...				TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTCTGTCTCCATTTGCCACGTCTTCCTC AGTAGAATAAGACAGGACTTTGCTGGTGTCTATCT/CJATTCTCTTCAGAAAGACACTTTGGCCCT CATAGGCAATCCATAGATATTTGTTGAATGAATGTGCTTTTGCATATTGATTCTCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55 A G ...				CCTCTAACAGAAACTTGACTTCTCAACTCAAAATACCCCTCTCTAATAATTTT/GJAGTAACCA AAATATCTTCAATAAATAATCTTTTAAATAGAAAGCAACAGTGTAGAGGTAGTACATTCA CCAOC

WI-9720a	47 A G ---			CCTCTAACAAGAAACTTGACTTCCTCAACTCAAAATACCCCTCTCT[AG]ATAATTTAAGTAACCA AAATATTCCTTCAAATAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---			CACGCTCTAAGGCAGGATGTGGCTTATGAGATACCTTTGCATTGTCTGTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTGCATGTGCAGATGAAGGCTCAGGGTGA/TJGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAAGTCAACAGGGTTTAGTTTGCAAT TAAGAATTGCCAGCTTTTGCTGCTGCATCATCTTGAACATTAAATCCACATG
WI-9748	74 C G ---			CCACTTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTCTAATTTTTATATGTTTACCCCTTT GTCATT[CG]TCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCCCTGGAACTCTTCAGAAT TACAGTTATGATGTCCTTTATATTCCTCA
WI-9943	91 T C ---			TGAGGCTATGATTGCAGATTTGTAGTGACTAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTTC[TC]ATTTTAAATTTCTACTGAGCAGAAAAAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTTAAATATGCAATTCACACCTTCTCTTTTGTCATTTAGGGA
WI-9891	39 T C ---			AGGGCCCTTCAGATCCGTCAAGCTCAACACTGCCTCTTC[CG]AGTGAGCCTGTGAACCCACCCAGAC GGCTGGTCATCAGTGTCATCTCTCTCTTTCCGGACAACATCTTTAAAGAAAAAAGAGTGT CTTTGAATGATCCATTTTATCCCCAAATAATCTGTTTAAATAATCTTATTAGGCCAAATCCAAT GTCTGAAATATCTGCCAAGCATGTCTTCTACACAAAAGGGATTGCAAA
WI-9897b	84 C T ---			CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATTCTGTTCTCAACATCTATTTTCTCAAAC ATTTATCTAGCCTGT[CG]TAAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---			CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATTCTGTTCTCAACATCTATTTTCTCAAAC ATTTATCTAGCCTGT[CG]TAAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---			AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGAGCTGGCAGGGGAGTTCAGACA[CG]AAGCCAAAGAAAAGCC TGATATTAAGAGGCACCTGCATTAA
WI-9935a	42 C T ---			AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCA[CG]TACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGAGCTGGCAGGGGAGTTCAGACACAGCCAAAGAAAAGCC TGATATTAAGAGGCACCTGCATTAA
WI-9983	146 C T ---			CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTAGGCTGCCTCCCCATTTCTTTGCTTGA TTCCCCAAACCCCAAGGTTCTCACCCTGATCAAAATGCTGACTAGGTCATGGCTGGTCAGGGTAA AGCATTATG[CG]TJAGACACAAAAGACAAAGAGGTAAGTTGCTGTCTCAAGAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGTTCTTA ACATTCAAAATAGATCTTTTCTCTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTAATTTCCCTAAGCACAGTAATCAAGGCTTCTACCCCA
WI-10020b	122	T A TTT	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCTGCTGACTCGTATTAAATAAATTATGTTAACTGGCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTT[T/AAAAAATACC AGACTAATGATTAAATAAATTAAACAGTCTAGGGTTCGGGAAGTGGCCTAAAGCACGTTAGTGGCCT CCTTAGA
WI-10020a	39	T C A TAAAT	TGTCATCTTGA CTCGTATTAA ATAAAT	AAATCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCTGCTGACTCGTATTAAATAAATTATGTTAACTGGCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTTAAAAAATACC AGACTAATGATTAAATAAATTAAACAGTCTAGGGTTCGGGAAGTGGCCTAAAGCACGTTAGTGGCCT CCTTAGA
WI-10064b	170	C T TTTACATG	CCTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACAGATAATTGGTGGACACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG[C/TTGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C A CAGGAAGG	GTAGCAGGAT CAGGAAGG	GAGATGCTCTG CAAAATTATAT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGTAGCAGGATCAGGGAAGGC[C/ATTATAATA AATAATAATTGCAGAGCATCTCTCTCTATGCACAGATAATTGGTGGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T C CAAACTCTT	TCTCTGTCCC CAAACTCTT	ATTCTTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCCAAACTCTTAT[C/TTAAATTCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T ATTCTTT	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACOC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATCTTTTATJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTTAGGTCTCTGTTTATAATTTGGTATCTTTTGGCACAAGAGTCTGTCTGAC AGTCTTATGATCTCTATTTTAACATTAACACTGGTCAGATGTGTTTAAACTTGTGAACCTGCAGC
WI-10316	104	T C CTCTT	CTGTTGATTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTTGACAACTTAGTGAGGTGTAATCAGAAAGCATCTATATTATTCACCAGTCACCCCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTTTAT[C/TTAAAGCTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCAGCC
WI-2572	61	C T ---	---	---	AGTGAGTTGGCACAAATTTGGAGACATTTCTGTGACCCCAACTTAAACACTCTCTCCCACAT[C/TJAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

WI-10368	31 C T	TGAAGCAACC AGGTCTGT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCAGGCTTTGTTTC/TCTACCCCTCTTAGAGAAATAAATAATATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTTCACCCCTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCTGATGGATTGCCTTTCAGGG
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTGTCTCAGGTATGACTCCCA/GTJCAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGAGCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACATTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCTTCTAATA	TGCGGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGCTTT CTAATAGCAA/A/CJAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	GGGTGCTCAAT AAATATTATT	AAAATTCTGTT GGTGAATAATC TAG	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAAAT/CJCTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	CTTTT	CTTTT	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAAAT/CJCTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	TACTTTA	C	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAAAT/CJCTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153a	33 C A	AATTATG	GTAT	CGTTGGGAATATTCTATCTCACCTAAATTAIG/CJAGTGATTAATAATATACATTTTAAACAACTTC AAATTGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGGATTTTTCATTTTCTTTAATA AAACATGCATATTAAAGTTGTCAGCAAGATGTACTTTAIGTTAATTAICTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	CACAAATGTA ACAAGAAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAACCCAGCTTAAATCACAATCAGCTTTTCTTCCCTGTA GAGCTCAAACTCAGTCTGAATGAATGCTGCACAAATGTAAACAGAAATGATCCTAT/CJACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAAGGAAACACACACAAAAAGTTTACCAGTGAATTATGACCAAAATGAGA/C/TJAAAT TTGTTAAAAAACCCTCAAAATGAAGAGACAAATATAGTTCAAAAGATTTCAGGTTCAATATTGT ACCTACAAAATAGGGATAGTCAATGGTGTGGCAGACTTTTCTTTTCTTTTGT/GJCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTTCCCTCTCCCCATATTTTAAAGAGAGAAATCACCTTTTCT CTGTGGATGATCAGAGGTTCTGCTCTTCCCAATCCAGAGGAGGTACTATTACCCCATGGGTCAT AGAGAGGATTAAACAGGGGTGATGCCCTGCAATGGGAATATTGAAAACC
WI-10656	59 T G	AGAGAGGATTAAACAGGGGTGATGCCCTGCAATGGGAATATTGAAAACC

WI-11169b	154	T G T T T T	T T A A C C A A G A G T T T T C A T T C	C T A A C T T A A A A A T C C T C A T T C A A A A T A T A A	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A A A T T A A G C C T A A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A G A G A G C A G A C A T T G T T A T C A T G T G T T C T G A T A A T T T T T T A T A T T T G A A T G A G G A T T T T T A A G T T A G C A T
WI-11169a	95	A G T T G A A A A	A A T A A G T G A A A G T A A C T G A C	A A A C T C T T G G T T A A A A A G C A C T A C T T	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A A A T T A A G C C T A G A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A A G A G A G C A G A C A T T T A T C A T G T G T T C T G A T A A T T T T T T A T A T T T T G A A T G A G G A T T T T T A A G T T A G C A T
WI-10685	25	A G	---	---	C A A G T G C T T G G A C C T T G G A T A G G T C A G A C C G G C T G A A G G T T G G A C A G T T G T T G G T T A G G T T G G A G A C C A A A A T C A G T C A T C C T G T A A T A T A G A T C T T G T C C T T T G G G T T A C C A C T A G G G G T C A C T A A A G A G A G A T G G G A G A C A G T C A A T C T T G T C T A A T A A T T C C A A A T A G C C A T G G G T T T G G A C A A A A T A C A A G G T T A G T G T C T C T A A C T T T A A T G G G C A T A
WI-10686	133	C T A A G G	T G C C C C T G T O C	C A A T C T C T A A A T T C A T G T G T A G A C A C A	A A T A A C C T G T G G C A C A T A A G G C A A A T A C T A G C C C C A T A C A G A G T G T T T A T G T T A A T A T T A T G A A A A A A G T C A A G A G A A C A A G A T A T A G T T C T G C T A G A A T A C T T G A A A T C T G A T G C C C T G T C C A A G G C T T T G T G T C T A C A C A T G A A T T A G A G A T T G A A T G A A A T G G C A A A T T C A G A A A A G G G
WI-11175	77	T A A	A A A T G A T T C T T T C T G C T C A A A G	C T G T T C T C A C A T T C T T T T T G A A A A	G G T A G G A T G A T T C T A G A A T G C C A C T T A C A G C C C A T G A A A T A T A T T G C C T C C C A A A T G A T T C T T C T G C T C A A A G A G T A T T T T T A A G T T A T C T A C T A T T A T A T T C T G C T T T T T C A A A A A G A A T G T G A G A A C A G T A C A A A A T G T T C A G T A T A G C A A A T T A A A A T T A A A A A G T A A G A A A A A A G A A G C C A A T T T G G G C
WI-10694	144	A G T A T G A G T T T C	T G C A A A T G C T T T A T G A G T T T C	G G C A T T T T G T A A A G G A G G A A A	T A G A G A G G T C T T T C A G T T T C A G G G T T G A G G G T G G T G A G G T G A G A T T C A C T T C T T A G A A G C A C T G G C T A T G T A C A G A A A G A T A A A C T C T G A G A A G A A C T C A G T T C T A A A G T G T T C A G T C T T T G C A A A T G C T T T A T G A G T T T C A G T T C C T C C T T T A C A A A A T G C C A T C A A T T C C T C A A G G A A A A A A A A A A A A G C T T T C T T
WI-2716	23	T C C	T G A A T T C A T C C A G A A A A A C A G	T C T C T T T T C T C T C T T G T T G T C A T T C	G T G A A T T C A T C C A G A A A A C A G C T T C G A A T G A C A A C A A G A G A G A A A A G A G A A T A A A G G T T T T G T A T A C G A C A A G T G G C T C A A G C A A T T T T C T G T C C C A G T G C A T G G A G C A G T G
WI-10719	115	T C C G C A T T C T A G	T G A C T C T C A A G G C C A T T C T A G	G C A C T G C C A G C A G C C	C A G G C C C A A C T C T G T C A T T A A G T G T T T A G A A C A G A C A C C T C A G T C A C A C A A A G T T C T C T T G T A T G T G C C C A C C A T A A C A G T T A C T G G A G G A T G A C T C T C A A G G C C A T T C T A G T T C G G C T G C T G C C A G T G C T T T T C A G C C T G C T G C C C A T A A C T A A
WI-10721	40	A G C T T G C C A	T G G C T C T G C T A C T T G C C A	G A A A C T C C C A C A T A A A T A A A T C T C A	C A A C C A A T T C A G A T T A A T T T T G G C T C T G C T A C T T G C C A A G A T A A G A T T A T T A T G T G G G A G T T T C T G A A G A T T C C C A T G G T A A T A G A T A T T C C T C T T C C C T G C T T A G G T T T T G A A G A A G T T G A A

WI-11204b	88	T C ---			GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACACAGGGAGTTGAGGTAAAGGGGTG AAAAAGAAAAACCTTCACCTTTT/C/JATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAAATTATTCAGAAAG GCAACATC
WI-11204a	80	T A AACTT	GTAAAGGG TGAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACACAGGGAGTTGAGGTAAAGGGGTG AAAAAGAAAAACCTTT/AJCACCTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAAATTATTCAGAAAG GCAACATC
WI-10732	80	C A ATTGGTTCACT	GCTGTGCTTC	AAGAACAATG CATAACAGAA CTTTAA	ACATGTATTTCCTTTAGTGGTCAAGCTTCCTTACCCCAAGAATATCCCTGGTTATTGCTGTGCTCTTC ATTGGTTCACT/C/JTTAAAGTTCTGTTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATCTCCA CACCACCTCTGTTTAAACTGTC
WI-11206	127	A T ACTC	GGTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGCTTTTCTTTGTACGAGTGTATATAAGAAATTACCACCTCTGTGCACATTTTGTAAAAAGATAGCACAG AGAGAAGCATTACAGGACGACAGCAACATGAGGTTGTGTTTCTGTATGTACAACTC/AJTCCAA CCATTAGGATTGTCACCTCATATATAGACAGAAATTCAGTGGTGGTATTGAAATCCACACATGGA ATAAGTCTA
WI-11215	68	C T ---			GAAAAAAGTTTTAATTGGATTGCTTAGTTTGCTTAAATTTGACCTACTTTTCAGATTTATTTTAGT [C/JATTTTTTCTATAATTTTCTGTAGTGATGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTATCCAAAGCCCCCATTCACCATGT TTT
WI-11219b	89	G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTGAGAGAATATCCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA/G/JAGAAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18	G A ---			ATGAAAAATGCATTAGAA/G/JAATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136	G A GCTGG	CATACCCTGC	AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAATGCTAAAAATGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCCTGTTGAACATTATGTTAAACATTTACAGCATACCACCTGCGGCTG G/G/JTCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTTCACAGGCTACTGG AAAGCC

WI-1122a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTTGG	AGCCACAGTGAATCATTACACTA/C/TGCAAAATCAGCAAAATGCTAAAAATGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCACTGCGG CTGGGTCACAACTGGCTACCGAGGAGAACCTGACACAGACTTCGTAATTCCTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTGTTTTATGCCATTAATTCATTACACTC/C/TJACATCATATTTTCTTAGCAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCCTGGCAGATAATCATATTGTTATCATAGACATTGCA GGAACCCACCATATGGATGGATAAATGTGTTTAAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAATGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/CJGACATAGTTGCTAAGGATATTCACAAATATAT TTCATGA
WI-11226	165 A C ---	---	---	CAGTGGCTGGCTACTGACAAAACGTAAATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/CJGJG TCCATCTCTGATGTACACAGCGGCCAGGAAGGTTGATCTGGAG TGGACACACTGCTCTAGACC/CJTCCAGGGTCCCTCAAGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGAGGCATCAGGGCCTTAGTCTCTCTGGGACAGTGAAGGGCCACCAACC ACAGAAAAATGCGCTAGGCTTGTAGCAAGAGAGGAAAGCATCTTCATGGCAGGAATTC/TJCATTT CTGTGTTCTTAGGGTTTGCGTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAATGATGA
WI-10778	62 A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	GGACCAACACAGAAATTAATTGGCAAT/CJAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATATTTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGA	TATGCCCTTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGATACATCTTCTGAATG GGCACATTAATCTGCAGGCTCTCC/CJTTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGGAGGATGAGAGAAGGGCTGCTCCGTGAATAC TAGTTCCG
WI-10810	58 C T GCAGGAAT	CATCTTCATGG GCAGGAAT	CAAACCCCTAAG AAACACAGAA ATG	GATTGAGTATTATCAAAATGGCCCAAGACCATTAAACAGATTTAATAGTTAAAGCCAAAACTATA AAGAAATTAAGTGTCAAAAGTGTGTTAAT/CJTCTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-10828	23 T C ---	---	---	GGATGATGTTCTGTGGTCCCTTTAT/CJAAAGCCCTCTTGATCCCAATGTGTAATATTTTATTCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCT
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	---
WI-10834	96 C T GTGTTAAT	AGAATTAAC GTTCAAAAGT	TGGCCCTATAA AATTGGTATTA AG	---
WI-2287	24 T C ---	---	---	---

WI-2296	81 A	G	TGTTACTTTGA TTCCTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGTTAGAAATGCAGGTGGCATCCTAGAAAGGTCAGGCTTTAGATAAGTTGTTACTTTGA TTCCTTGCTCTGAC/GGCCAGTTAGCTGTGTGATTTGCAGAGGTTACATTTGTTGTTG
WI-2300	77 G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCCCTTATTGAGCGGGCAGGTGGTAGGCACAGAAGC CAGTCATAC/GTJGCTTTAAATTTGACCCCAACCACTTACTAAGAATAGCATTCA
WI-2371	55 G	T	GTCCTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCAACATTTCCAGGGAAGGCTGGCTGTTCTTCCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTGACATTCCTTGCTTGACGCTGTATAATCCCAATCCTTGCCCTCCAGCTTTACATGATGT TCTCTCGGTGCTGCTG
WI-2395	122 A	C	GAACATAATT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA	GGGGGCACAAATTTAGCTACAGTGCATATTAAGAGATAACATAGAAATATCATATAACTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAA/ACJCTGAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTTAAAGAGCTAAATTTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G	A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G	A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G	A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTCTAAATAATAGACACCAAAAAATTTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G	A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAACGGGTCTCTCCTTAGACCCCTCCAGAAAAATATGCAACCTACTGACAAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T	C	TGTTTAGGAA ATAATGACAA	TGGTTACAAC GTACCAACAT G	CTGTAACCTACACACATCCTCCTGTAACTCTAGGTTACTTGTAAATACAAACACAAATGTAAATGCT ACATAAATAATTGTCATATACTATTTAGGAAATAATGACAGAAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCAATAATTTCAATCCACAGTTGGTTAATCCACAG AAACCACGAATG
WI-2886	46 C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAGA[C/A]ACGAGATAAAGCATG GCAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCATTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGACAGAAACAGAGGCGTT

WI-2906b	77	T A	---			CCTGAACACCTGGAGCACTCCCTCCCTTGGACACCTTCATTCTTGCTGGAACTTGCCTGGAATGCTC TTTCCCTCTT/AJGAGCTTTTGCTTGGCTTACTTTTCTTTTCTTTTCTTTAGGTTTCAAGTGCACCT CCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50	A C	TCTTGGTG	GACACCTTCAT	AGAGCATCCCA GGCAAAGT	CCTGAACACCTGGAGCACTCCCTCCCTTGGACACCTTCATTCTTGCTGGAACTTGCCTGGAAT GCTCTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAAGTGCACCT CCTTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175	C T	---		---	TACTCCTCATTCCTCATGTCCCTAGACGTACTCAGATTCCATGCCCTGAAACATTTATTTCCCTAAAT TAGATTTCCACCCCGCAGCACTATTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGA GAACTTACTTAAGGACAGTGGTTTCCATCTGCTTCCA[C/T]JAGAGATCTAGGGTGTCTTTGGAACC ACCTTGG
WI-1851	136	G A	GTGTTAAGTA	GCATTGAATT	CACTAGCAATG TTAAACTGAAG TTG	AATACCCACGTCCTAACCCATCACACTGATCATCAATCAGGTTTAAACATATTAAATCTGGGGAGG ACACAAACATTTAGACCATAGCATTGAATTAACATATAGATGTGTTAAGTAATTATTAACATGGTA CA[G/A]JACAACTTCAGTTTAAACATTGCTAGTGATCCATGTGGATACCATGTACCTTCTTACATCATG TGA
WI-3000	62	G A	AGAGACCCC	CCCAAACAC	ATTGACTAAGA CTCA	CTGATGTTGGGAAGCACTGCTTACATCTCTAAATGTCAGCACCCCAACACAGAGACCCC[G/A]T GAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTCCCTGGTGCATAGTAGACACT
WI-1754	177	G A	TAGTC	CTTAAAGAGA	AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCCAACCCCGGATTATTTTACT TAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTT TTCTCTTCTGTTTGTGTTTCTCCCTTCTTAAAGAGATAGTC[G/A]CCAGAGGCAATTCGACTTTCTGT AGCCACAAGATT
WI-3167	37	T A	TAGATT C	AAATCAACC	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAAATTCACCACAGATCTATTAGATTCT[A]CACCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G A	AGATAAAGA	GTGGAGTGGGC	TCACTCAAACT AGGCTTGG	CAAGCACACATTCAAGGAGTGGGAGGTAGGGAAGGTGGGCAACTTGGCAGCAGAGAGGAGGAAG AAGTTCAGACCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGCAG ATAAAGA[G/A]CCAAAGCCCTAGTTTGGTGGACACTGTGGGGGATTCAAG
WI-1775	47	C T	TTTCTCTG	CCTGCATGGTC	AGTTGAGATT ATGACAAATGAT GTAA	ACTCCACCACAGTTTGTGAGCCAAACCTGCGATGGTCTTTTCTCTG[C/T]TTTACATCATTTGCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55	G A	ACAT	AGCATATTCA	GAGGACTTAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCCCTTACAT[G/A]CAAAATGCTC CTTTTAAAGTCCCTCAACTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCTTAGGA

WI-3416	33 C T	CCAAGTTGTA GCATTGAGAA	ACGAGCACAA CTACCTCTAAG AG	TC TGGTTCCTCCAAGTTGTAGCATTCAGAAGTC/C/CTCTTAGAGGTAGTTGCTCGTCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCCAAACAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGACACAATAATTAATCCCATTCGCTAAAAAGACCAGG
WI-3453	70 C T	TTC TAGGCC ATCAGAGAA	TCAATTTCCC CATGACTTC	TCCTATTCTACAACAACAGAAATTTAACAAATGAAATCAGCTACTCTCTTAGGCCATCAGAG AAT/C/T/GAAGTCATGGGGAAAATGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAATCATCAAGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT/G/A/TGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCGA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAATCATCAAGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCAC/A/G/JTATTTAATGAGGTGGTGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T	CCTGGTTTCT GGATGTCT	GGGTGAOCCGTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCAATAAGAAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCT/C/J/TGAGGACAGGGTCACCCAC
WI-3600b	146 G C	GGTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/G/JGAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT/G/C/JATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3600a	78 T G	CCATGCCOCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/G/JGAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3678	125 G T	---	---	TAAATCATGCTTATTTTACAAGGTAATCCACTCACAATAGGCAATTGATGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTGTGTATGATGCACCTG/J/CCTTTTGG ATAGATGGTTGATAGGAGATGGGTGTTAAAGACACAATTTACCTTGTGTGTTTCAGGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTCCAAAGCCTTTATGCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T/A/C/JAAAAAATCTATAGTTTATGAAAAATGACTTCCAAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAATCCAGAAATCTCTGTCATTTCTTAACCTTTGACTGACACAG
WI-3735	72 T C	CCTCAGTTATG TATCAATGA AAAC	GGCTCACCAT CATGTTTTT	TCTAAATGTGAACCAAGAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGATCAAAATGA AAAAC/T/CJACACCGGTTCAATGAAAAAACAAATGATGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGCAATTAAGTC

WI-1819	51	C T	...			GAAAAAGCAGGAAGCCAGGACGACAAACTTTGAAAAAGTCTTTAGCAAC[C/T]TCGTGGATCCG AATTTAGTGTGATTTGGCAGGAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAATGTGGAATAAAAAAGGGTGGTAACCTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116	G A	...			GGCCTATTACATGACACTGGCCAAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
				ACAGTCATTT AGTCTTCCCTGA	TAAGATAACC ATACTAGGTAC	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGAACAGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C G		TGACCAATGTC TTTAGAAGCA	TCGTCGGTGTG CTCTCC	CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCAAGGAGGAGGAGCAAGGGTTGCTGGCCACT
WI-3901	114	A G	...			GGACCAATGTCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAAACCTCGGCTTCTCACCTGACAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTATAATGCTGCAT
WI-3914	99	C T G		TGATTCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACTGAGGAACTTTTATTACCTCCCTGAGTTTGTGCCCTTGCAA GACATTGCTGATTCTTCTCAAGACTCAGAC[C/T]ACCATCCTTCTTCTGCTTCTAGACCTATAACTAG ACTCAAGTCCCAGAGGCCCTTAAAGGTAAGGTACAAAGTGTGACCCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A A		CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTGTCTCTGTTATTGCTGTTCAACAGAT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTATAGATGCTGCAGGAGACGAAGGTC
WI-4091	84	A T		TTGAGGTCTTA GTCATTGCATG	TGAGTTCTCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTGTTTGTGCAATTTATTGCTTCTTATGTAAACACAATCACCAACATTGAGG TCTTAGTCATTGTCATG[A/T]GTATAACAATATTGTCACCTTAATAGGAACTCAAGCATAGTTAIGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G		CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTCTCTGTAAAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGGTGGCTTCTAAGATGGTAAT ATCTGTCCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCTCCCTGGATCTGAACGTTCTTCATGATAC
WI-4168	32	A G AACA		GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAAATATACCAGCAGTGGTCTAGCAATTTCTGCTGGGCAATTACCTAACATAAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCATATACTTTCCAAATGACTAGTATGAATAAGCACGTTAAATTTTACCTATTATATTT AT/C/CATCATGATTGCTGCCCTTCTTCCAAATTTACTACAAATTTGATTGTGCACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A C	CTCCCCAAGTT AGTCAATATA CAAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACTCCCAAGTAGTCAATATATAAAAAA/C/CACACACATATTG TTATACCTAATCAACATATAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24 C T	CTGTCACTGGT CTGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGCACCTGGTCTGCCCTG/C/CTGGTCTGTTCCCTGTTCCCTTTCAATGTTCACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTTGGGCAT
WI-4250b	117 A G	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGTCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAACAGGGGTGGGAAGGATCCTGTAAAAGG/A/GTAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAC AGG	CTTTTACAGGA TCTTCCAC G	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGTCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAACAGG/G/CTGGGAAGGATCCTGTAAAAGGATAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G C	TGCTCCCCCAT CACCT	AGTTGTGTAAG G	TAAATGTCTGGGGAGATAATAGGAAAGGTCCCATCCCTCTGATACCTTGTGCTCCCCATCACCT [G/C]CTTACACAACTTGAAGTAGGCCCATCCAAACACTGTGTCAGAGAGTAATACTGTCCGAC
WI-4256	57 C T	ACAGCCTCTTCAATGGCACAAATCAAAAGCACCAAGTCAAAAGCAGAGGCAAAATCTGG/C/CTCAC CATGGAAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT
WI-4325b	71 C T	AGTTCACTGCCTAGATGAGTAGACCATTGTGCTTTTAAATGACTCTTCTTCAAGATATCACCAGCCAC GATG/C/TTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	AGTTCACTGCCTAGATGAGTAGACCATTGTGCTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4347	158 A G	TGGGAGAAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCACTTCTGCCTGTCACTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCTCTGAGTTTATCATCTCCACCTCCAGCCAG GGCCCTGTATCTGTCAGGGCC/C/G/GAATCGTCAACGGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-1936	117 T C	CCAGTCTAGGCTGCAAGGACTTCAATTTCTGGGCAAGTCTGGGTGTGTTGTTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACCAGTGGGACACAGGGGTACTTGTATCACTT/C/CTCCCCGAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAGGAGAGGGGAAGAGA AAAGAGGACTTTGACACACAACTTGA

WI-5204	54	CT	---	---	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTTGTTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGCGAGAAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTGG
WI-5215	70	A	G	CTCAAAA	TTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCCTTAATATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAAT
WI-4448	112	T	G	ATATAA	CCCTGAAATGTCCTTCTCCTCCAACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTTGA AGAGTACTTTAATTAACCTTGATCAAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTCCACTGCTATCAGTAAA
WI-4456	49	CT	TATAGTTCC	AGTTGAATTA TTCAGAAAT	ACACATTTCAATTTGCTTTAAGTTGAATTTTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTGGGCAATTGATTGAATTGT
WI-4461	49	A	G	CTTCC	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAATATCCTTCC[A/G]TGAAATTTGGTGAAA GGTCAAGAAATGAAATTTCCACTTTTAGATTTCTGGAAATTTTATTTGGATGATAATGCAATGGGC
WI-4465b	75	G	A	---	CTACTGGATTTTACTTTGCTCAAGCCAGACAAACGAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT TCACCTTT[G/A]TATTTCTCTTCTACCTCAGGGAATC
WI-4465a	41	A	G	ACACGAAAGT	CTACTGGATTTTACTTTGCTCAAGCCAGACAAACGAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGTATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160	T	C	TAATC	GGGTTAGGACCTCGAGATCTTTCAGAAAAGCACAATTCAAACCATATGCGAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G]CAAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT GAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCGCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86	T	G	ATGCTCTGAGT	GGGTTAGGACCTCGAGATCTTTCAGAAAAGCACAATTCAAACCATATGCGAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G]CAAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCGCCACCTCTCACACCTTTCCCTGG CACA
WI-4529	64	T	C	AAGATG	TGAGAGAGTTTTGGATTATTCATCTCTGCAACACTCCAAAGTAAAGTCTATCATTTGAAGATG[T/C] GAGTCTCTTTTATATCTCTATGATTATTTTTCAGGAAGTGTATTTTAGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGGTGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110	A	G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTCCTTTCTTAAAAATGGTGCCATAGTACTGGCTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCCGAGTGATGGCTGCATTGTCCAGTC AAATGAGACAACCTCCTAT
WI-4582	226	T	C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCCTGTACACA AATAACTTTATGGGAGACAGCATTGTAATCAAAATCAATAATGACTCGGTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTTTCCTCTTGCTAGAAACCATTTGAT
WI-1965	105	G	C	AG	GAATGGATGGG TCATCTCTCT	CAAAGTTAGTTTAACTTGGGGGCAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAGG/CJAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCACACAGATGTGGAGTCATTTATTTGGTTGGTGATGACAGT CATGG
WI-5248b	99	C	T	TTG	AGAAAAAGAG AAGAAAGGAA AAA	TGTTAAAAACCATACAGTTTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAACACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/CJTCCTTTGCTTTTTTCCCTTCCTCTCTTTTCTG CCCTCTTTAACTAT
WI-5248a	38	G	C	CTACGTTGTT	TTTTAATTTT TGGGGTGTCT	TGTTAAAAACCATACAGTTTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAACACGCCT TACCAATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTGCTTTTTTCCCTCTCTCTTTTCTG CCCTCTTTAACTAT
WI-4596	69	T	A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTGCCAACTTCGGTGACATTACTCTGTGACTTTGCTCTGAAGCAAGAACACTGTGA C/T/AJCATATTATTAGGCCCATCTCCTGCTGAGCCTGCCTACAGCAATTTGTACATATGGCATTGGG ACATATCTCTGAGCCCATCACTATTTGACAAGATTCTCCTTTTTTAACAA
WI-5252	119	A	C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAAGTCTTGGGAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATACGTAATACCTGTGTGAATCATTTGCTTTTJAVCTACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61	A	G	CT	GCAATGCTAG AAAATTATGC	TGCAAAAAGGAAATGATAACCAAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCTTAJAG/C CAAGTAGACAACCTAAGCACCTAAGGCAGAAATGAAGTTTCTCTTGTCAATTAAGTCTCTATTCA ATTACCATTTATCGGGTAATTAACACTGGAAGTAATGCCAGGCTAATGTTAGATTATGATAAT TACAGTCTTTGCTATGCT
WI-5257	77	C	A	GCAAGAGG	OCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAATACCAAGTTTGGCAGAGGCATG AAGCAAGAGG/CJCTTCATCTGCCCTGGTGGGTTTTTCAGTAACCTGCAACATGCTTTGCTCC CGGATGAAAAGATACCTTCTATGACTCAGCAATTCACACTCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50	C	T	TTCCGAATG	TGACTAGGTG TACTTACAGA AATCATC	TCACTGTTTAGAAAATTTCTTCTCTCAGTGAGACCATTCTTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTG G	AACTGTGTGGTATGATTGTTGTATTTTCTGGAGAGTCAGTTACTCTCAGTATAGATCAATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAAAGCACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACITTCAGTAACGTT
WI-4677	82	T C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTGACATTTTGGAAAAATTTGCCAAAAGTATTAGGTGAAAAAAT GAGTTGAATAAATGTT/CJAAGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C G	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTTCACCTGGCAATTTGACCTGCAATTTCAATTAAGTTTGTC TCACCTGGGAACCTGCTTATCTTGATGTCAGTGACATTTCTTTTGTGACGGAAGAAAACTTCAA C/GTTGAGAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G A	TGCATATGG AACACCAC G	AATATGGAATC TGCATTCAGTT G	CTTCCCATTTGCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCATATGGAACACCACAC[G/A]CAACTGAATGCAGATTCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACTTTGATGGTTGAGATTTTCAAAAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACAGCAGTGTGTCTAAAAAATATGATAGTTTCTTCTCCTGTGCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T C	TGTTACGTT CCTGCTCATC GAA	GGTTGGAACT CAAATTACCTA GAA	GACTACAGGCACAGACAGGCAATGTGTGGCTTGCACAGGTTTGGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAGTTTACTACAGACCTCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCTCATC[T/C]TTCTAGGTAATTTGAGTTTCCAACC TGTGG
WI-2033	183	T C	GGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTOC	ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATTTCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAAATTTTAAATTTTCCAAGTTATACAGGACAGTGTGGAAATTT AGCATTTCTGGGTTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCAT[C/G]GGGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCCCTCTCCACCATTCTCCATCTACTTTCTACTCTGAT[C/G] AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T C	CCACAGTGCA CCAAGGAC CC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCCAAGA CCTCCTTCTCGGGTTTCACTGAAAGACGATGAATCTCTTCTACAGCAGCTGGACTTCAACCA CAGTGCAACCAAGGAC[T/C]GGACCTGCACCTATCTTTACCCCTCCGACACCCAGATGCTGAGATGCC ACACTCTGAGTG

Accession	Position	Sequence	Accession	Position	Sequence
WI-5370	143 TC	AATAAGATGG TACCTTAACTA ATAAAACAA	CAAAGTTGGTA CAGAGAATTTG AAA		TGCATGTTACTCTCTTGGAAATCATAAAGGGATCTGAGAGCCCTACAGTATATGGCAACATTAAACCAAT CTTTTGAAAAATTTACCTGTATCCCATCATGTTTCATTTGCAAAAAAATAAGATGGTACCTTAACCTA ATAAAACAAATTC/TCTTGAATTCCTGTACCAACTTTGCTTTTC
WI-9711b	423 TA		---		GATCTCTTCATCCCTCCAGAAGAGGAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCC CCAAATCTCTACCTCATGGATGTGAATGCOCCAGGTGAGGAGACGGCTTGTCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTGTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9711a	390 CA	---	---		GATCTCTTCATCCCTCCAGAAGAGGAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCC CCAAATCTCTACCTCATGGATGTGAATGCOCCAGGTGAGGAGACGGCTTGTCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTGTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9702c	345 GA	---	---		GGAGGAATTTACGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTGAGCAATTCCTCTAGTGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTAAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG
WI-9702b	344 CT	---	---		GGAGGAATTTACGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTGAGCAATTCCTCTAGTGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTAAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG
WI-9702a	179 CT	---	---		GGAGGAATTTACGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTGAGCAATTCCTCTAGTGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTAAATGATCTCTGTGGA CTTTTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTG
TIGR- A003N21	49 CA	---	---		TATAGTATTTAACGAAGCCTAGAACACGGCTGTGGGTGGTGAATTTGGTTC/AJAGCATATCTTAGGT ATATAATAACCTTTGAAGCCATAACCTTTAACTGGAGTGGTTGATTCTTTTAAATTTTATTGGGA GGGTTTGGATTTTAACTTTTAAATGTTGTTAAATATAAGTTTTTGTAAAGGAAACCATCTCTG TGATTACCTCTCAATCTATTGT
TIGR- A004V30	203 CT	G	---		AGAATGGCTACTTCATAGGGCAGAGCAGCCACTTTTGGCTAATTTTAAACATCCAAAGCTAATAAAT AATCAAGAAGAAATAGAGAACATTAAACAAAAATAAATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACCAAGTACAGTGATAAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGCTGCTCTCTAGGTTAGTAAAGATT

WI-7593	46 G A ...	---	TTTGTGTTGCTCTGGACACCCCACTGCTCCAGGATGAAGGAGAG[G]AATGAGATCAGTTTGGG CACTTCTCTTGAATATAAAGAAATCAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G ...	---	AGTGCATCTTGGGGAAAGGGCTCCAGTGTATCTGGACCAGTTCCTTCTATTTTTCAGGTGGGACTCTT GATCCAGAGA[G]GACAAAGCTCCTCAGTGAGCTGGTGTATAATCCAAAGACAGAAACCCAAAGTCTCC TGACTCTGGCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCTCATTCCAC CTATCTCTGAAATATCTCTGAGAGAGAACAGAGATTAGATAAGA
WI-7059	43 C G	AAGCACCCA GCCATC	GCAGAGAAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC[G]TGACCCAGCGAGGAGGCCAA CTATCCCAATATACCTGGGTGAATATACCAATTTCTGCATCTCCAGAGGAAATTAAGAAATAAA GATGAATTGTGCAACTCTTAAAAAA
WI-9063	53 A C TT	CACTTCACTGA AAGACACCAT	AGCAGCCATCAGATGATCTGTTTTTACCACCTTCACTGAAAGACACCATTTAT[A/C]TACCCAAAGGG CAGAAAGTAGAACTTACTATTCAATTAATGTTTGACACAATTTGGAATTGTC
WI-7079	293 T G ...	TTTACTTTCTG CCCTGGGT	AAGGGCATTGAGACTATAAGCAGTAGACAAATCCACATACCATCTGTAGAGTTGGAACATGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTTCTTATTTCTTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTAATTACATTTATACATCACCTTTTGACTTTTCCAAAGCCC TTTTACAGCTTGGCAATTTCTCGCTAGGCCCTGTGAGGTAAGTGGAT
WI-9074	38 A G AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAGTTCTTTTGTCTAAAAGAA[G]AAGGAACACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTAATTTTAAAGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249 C T ...	---	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGAGGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCATCTTTG[C/T]
WI-7104	157 C A ...	---	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGAGGCC CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCCCTTGCAACAGGTGGGGCCACAGCACAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T CTTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTAACCCCAACCTCATTTTAGTTGCCTAAGCATTTGCTGGC[C/T]TTC CTGTCTAGTCTCTCTGTAGCCCAAGAAATGAACATTCCA
WI-9014c	93 T C ...	---	CCCTGTCCCATGCTGACCTGTGTTTCTCCCCAGTCATCTTCTCTGTTCCAGAGAGGTGGGGCTGGAT GTCTCCATCTCTGTCTCAACTTAT[C]GTGACACTGAGCIGCAACTCT

WI-9014b	44 C T	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCTCCAGTCATCTTTTC/TGTTCCAGAGAGGTGGGGCTG GATGTCCTCATCTGCTCAACTTTATGTGCACTGAGCTGCAACTCT
WI-7023b	206 C A	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTGTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGATCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGTCCCC TCCTTTTGGCCCAATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/A/CACACATCTGCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTGTGACAG/A/C/CCTGGGT GCTCAGTGCCCTTTAAGTGATCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGT CCCTCTTTTGGCCCAATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTGCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T	---	---	CTGAAATCCCTCTCTGCTGGCTGGATCGGGGACCCCTTGGCTTCCCTTC/TGGCTCCAGCC CTACAGACTTGTGCTGACCTCAGGCCAGTGTCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAGTTGTGAGCAGAGAAAGCTGGAGGAGGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTAATATTGTTGCCGCTGTGTTGTTGTTA
WI-9171	62 G A	---	---	ACATATCTGAAAAATGTTGAAAGCTTAAGCCAGGATAAAGAAAGTAGAGATAATAATCA/G/A/ TCTTTACAACCGATGGTAATTAAGCTTGATTCACAAGACTTCATGC
WI-9174	47 T C T	CTAGACCCC ATTCTCCTATT	TCTAGAGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTAT/C/CAGTCTCTGCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA	CAGAGGCTTG AAATACAGGG A	AAGCCAGATGCACATCCCTGGAAGGACATCCATGTCCGAGAGAACAGAT/A/GJATCCCTGTATT TCAAGACCTCTGTGCACTTATTTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A	CCACTTCTCCC CGCA	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCGCA/G/A/JACCTAGGTGACACTTCCCTTTCATCTT
WI-9193	94 G A	AGAAATTGT CTGCCTTAAAG CA	GGTGTGTGG TAGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGATAA CTCAGAAATATGTCTGCCCTTAAAGCA/G/A/JATCCCGCTACCACACACCCCTGTCTC
WI-9015	48 C T	---	---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATGGGCTGGATTG/C/TGGCTTGGTTAATACAT CTTTCCCTAAAGAAGATAAACACAAAAATCCATTCAGGTAGCTCGGACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGCGGTCTGAGAGAGGAGCCAC/A/GTCCCTAATGACACCCACTCTAGCC CTGAGGCTCGTGGCCCTCAGACTGGGAGAGTCCAAGGAAGGGAGGAGGAGCCACTCTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 G C	CAGGTC	CACCTG	GTGACCCCTGTGAGGTGAGTCCGCCAGATTGAGCTGAGTGGGCAAGTGTGTC
		GATTGA	ACTCAGAC	GTGACCCAGAGATGAGGCTGAGAGCAGGAGTTGAGGCCGGAAGATCA
WI-7836	120 T C C	CAAATAAACA	GCTCAGAAC	TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCAGTAGTACTGAAAGAAAACCTCTGCTA
		ATGCAACGTTT	CAAGATTAGA	GAATGATAAATGTGATGGTGGTCTATAACTCCAAATAAACAATGCAACGTTCTTCGATTCTTAAT
		C	AATC	CTTGGTCTGAGAGCCATTGGTTTCAGTTGTAGCAATCCCCATACCAGCT
WI-7286	65 T C A	CAGCTCAGCT	AAACAATCTA	TCATTCTTTTGGCCCTGCAGCATGTGATGCTCCAGAAATTCAGCTTCAGCTTAAGTACAGATTC
		TAACTGACAG	ACCAGAAAGCT	GTAAAGCTTTCTGGTTAGATTGTTTTCAGTTGGTGATGATGCTTTTCCATGTGACCTGTATATAT
		C A	TTAA	TTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT	CCCAATTTTA	CAAAATCTTGGAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT
		ACGTGAATTT	TTAAAGTTTA	AAGCATGTACGTGAATTTTAAATTTGATATAGATGTAAACTTTTATAAAAAATGGGGTGTGG
WI-7860	50 C G		CATCTAT	GAAGATTAGGGAGGGTGTCTGTGGTCTCTCCCTGCCCTCTCCCAACCA/GTGGGGAGAGACC
		A		TGTGATTTGCCAAGTCCCTGGACCTGGACCACTGAGCTGAGCTTATGGTTGGGGTGTAGGACAGG
				TGAGCGTAAGTGGGAGGGAATGGGTAAGAAGTCTACTCCAAACCTAGGCTCTATGTCAGACCCAG
				ACCTAGGTCTCTCTAGGAGGGAACAGGGAGACCTGGGGTCTGTGGAT
WI-9064	29 A G TTC	CGTACCTCCAA	GCCTGAGTGA	CAAGCGTACCTCCAAACATAATTGATTC/GATATCTGCGAGACTTACACTCAAGCAATCCTGAGG
		ACATAATTGA	AGTCTGCAGA	AATACTGAGGAGGGCTGGCTACTGCTCTGCACTGCTGCTTTG
WI-7307	128 G T			CACACTGTCTGTTCTCAGTGTGAGGTCTGGAGGTCTGGCAGGTGAGGTGGGTAAAGCCGGGTCCACA
				GGCCCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGCGGAGAGCAGTCCCTCCCTCAG/GTAACT
				GGAGGAGGGGACTCCAGGAATGGGGAATGTGACACCCATCCTGAAGCCAGCTTGACCCCTCCAGT
				TTGCACAGGGATTGTCTGGGGGTGAGGGCCCTGTCCCAACCCCGCCC
WI-9274	25 C T G	GAAATGTGAC	CAGGTAGAATT	GAGGAAATGTGACTTCACCTTTGGTG/C/CAATGAGACAGAAAATCTACCTGTGCTACATAGGAGAA
		TTCACTTTGGT	TTCTGTCCATT	GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTTCGAGGTGGAAA
WI-7313e	266 T C		G	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTGGTCTGATTAGTTCCTTAAT
				TGTTTTCAGTCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATCCCTTATCATATCTTTAT
				AATTCAGCCAGTGTATCCACAGTTTGTGTTTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG
				AAGGTGAATATCGTTTGTGTTTAACTGAATAGATTGTATAGCGATGA
				AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTGGTCTGATTAGTTCCTTAAT
				TGTTTTCAGTCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATCCCTTATCATATCTTTAT
				AATTCAGCCAGTGTATCCACAGTTTGTGTTTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG
WI-7313c	256 C T			AAGGTGAATATCGTTTGTGTTTAACTGAATAGATTGTATAGCGATGA

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA AAAA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGAGGGAAGCAGAGATTAGAGAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTTTCATTCTGTCATTCCAAGAGAGAGGAAAGAAAAA T/AJACAACTTTCATTCTTCTTTGCACGTTTCATAAACATTCTACATA TCCTGCAAGAAGTCTCAAGCCTTTTGTATTTTGTGCAATAAGTACAGCTTTTGCAATAAGAGTGAAA TTGGCTAGCTTAAATGGATCCATAAACTTCTTCTTAATTTAAGTGAGAJC/TCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAACTCAAAATATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTCA GTGGCCACTACATGTTATAGAAACCATCATCTTGTCCACAGCAGCAGCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCAITAAAGGTGCCCATTTAAAGGACTTTTAAATCAACCTAA TAAACTCTAATTCGTGACTTTTTAAAGATCTAAGGTCAITTTAATACATGCTGAAAGGGTCACA ATTAATCTTTGATCTTTTTACTCACTGTTAACTTATATAAT/AJTTCAGAAC TACAAATGAATGCTTTTATTTCGGTATGCATCCACATTTTCAGCAITTTAGTGTCTCTGAACAGCAAG TGGAAGACGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTTCGGGATCTGCTGTGCACACCGG GTTCCTCTTAATCCCTGCTGAGGATCTTG/AJGAAGCAGCAGCAGCACCACCAAGGCATGCA CCGGATTCAAGGTCITTTTGTCCAGTTGTCAGATTCCAAACTAGACCCCA AAGATCAACCACCAACACATGACAACCTGCCAGGCAAGGCTTGTCTCCCTCCCTCTTTCGCTCC ATGTGCTAGTCAGCAAGGTGGGGAGGCACCGATGTTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAAJG/CJGGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACTGGTATGCTGAA ACCAAGAGATCAGCTGTCTAAACAGAGCTTTTGTATTG/TJGGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACCGAACCTGACCTGAGAGGGGATGGGGCTCTCTCACA GAATATTTGGGGCAGAACCTGGAACCTGGCCACCGGACATCCCAATATCCCTCCTCCTCAGGG CTACCCGACATCTCAGCCAAATGAAGGCTCGAA GGGTGAGACGGGTTATTGTGCACATTTACACAGCGTCACAGCTGTGGCTGGCAGGGCCATGCTC CTGTGGTGGGCTGCTCACAAGGGCGTTTCACTTTTTCACCACTATGTACAGTCAAGTGTCTCAA GGTATGGGCTACAGTGTGCTGATGAGTGTGTACACACATTTTACATAAATTACACAGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCTGTATTTAATGAGAAAAA AACTGTTTACAAAATAGGCTTTCAAACCTTCACTACTGAATGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCAGAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG TG/AJGCATCTTCTCACCTTAAGTGCAGCTGCAAGATGCCTCAGTGIG
X86400	118 A C	---	---	
WI-8053	242 T A	---	---	
WI-6190	165 G A	---	---	
WI-6275	148 G C	---	---	
WI-6421	41 G T	---	---	
WI-6905	215 T A	---	---	
WI-9420	202 G A	---	---	

WI-9448	184 G A ---	---	TGGGGCTGCTTTTAGACTTCATTCTAGAGCAGACACCTAGTAGAGGAATACCTGGGAGAGAGAC TGCCCTGCCCATGGTGGTTAACTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTGGATTTTATCCAAGCGCATGTTCTTAACGTGCCGCTGAGCAG
WI-9470	204 G A ---	---	ATGTCAGAAGAGACACAGACAGAGTTTTCCTTTTAAATGCTAAACAAGTCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCCAGATTCTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACAGGGCTCACCTTCCCAAG
WI-1245b	201 G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTCCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGTGGT TTATTAATTTCAATTATCATCTGGACAGCCCCCTTCTTATAACGTACATCCTTGGCCTCTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85 T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTT[G/C]GCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGGT GGTTATTAATTTCAATTATCATCTGGACAGCCCCCTTCTTATAACGTACATCCTTGGCCTCTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149 G A ---	---	TCAGTGATAAGGACAGGTCTAGAACAGCGTTCCCAACCCCTGGCACCAATGACAGTTTGGACCAAA TAACCTTTGTTTCAGGGGACTGTCTACACATTGTGGGATGTTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCAACAATCATGACAAATGAAATGTCTTTAGACATT GCCAAATATACCTTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110 G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199 T G ---	---	ACCAAAACCGTTGGCAAGGCTCCCCAAGACTCACCCACCCCAACTTTGGTGCTTACCCATGCCGGGTG GGATTGAAGAAAATAACCATAAATATAATGCTACAAATTTTCCAGTAGTTACAGGCCACCGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGTATTGCTCTCTGGCTTGGTCCAGGCATAGAGTT/G]GGCTACAACCCATTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157 G A ---	---	TGGTATTTTTCCTTTTCCATAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAAGTATAGTTGAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGAATGAGAAAAAGCACACCAAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAGTTAAGT

WI-1968	167 A G ---	---	TGGTGAGGAGCTGTAGGCTGAAGAATAGTCTGCTGCTGGCTTCGTTGGAAATGGATGAGTCTCT TTTACAAAATTTTCCCTCGCATGGGTGTTAAGTTAGAAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGT/GJ/GJGAACCTTGAGCAAGTGCTCTTAAATGCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCAATTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAATAGGAAGATAG AAAAATGGTGCCCACTATTGACTTGTAAACACCTACAAAACAACACATTAACTCCTCCCCACTCTA CCCGCCAAAGTCTACCTTTTGTTCTTTATTTCTGCTAATGACCATACTATTCCCAATTAGAG/GA CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTCCAAACCATTGTGTGTTTCTTCACATACCTTTACGTAATTTAAATCATGTCATTTAATTA TGCATTTACTTGTGGCTACCAAGACATTGCTTCCAATTGTAAATCCCTAACACAGCAAGCATAACT GATGTGCCATCTTGTATTCTCTAAAC/C/AAAGAAAAGTGCTTTTGTGCACTCTGCCCTCTCTGT CTTCTCTGTTTCACTCTGTATTCCCTATTTCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACCTTCATTTGACATTTAAGAAAGATAAAGAAAACAACGATCCACTGTGTTTGCTT GATTT/GJ/GGAGATAAAACCTGATCTCTAAGAAAATTAACCAAGCAGTACACTAAATAGCCT TTGTGTGTGGTTTTCAGGAAAGAAAGCCATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAAATATAGCA
WI-9705	111 C A ---	---	TGAAGGACCAGTTTGAATGCCTACCAAGGTAAAGTAAATCGGAGGGGCGAGGATGAGGTTGCTT CCGGATGTTGCATAAAATCAGGTTCTTTAAGGAGTTCGGCTGCC/C/AAAAATTTTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGTAGATTGCGGTTCCCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATTTGTTGCTGTGTTCTTGGTG
TIGR- A004248	177 A G ---	---	CAAATAATCTCTGCTTAGAAGTTGCTTAGGGCCATGGATTCAATGAAGGGTGGGCGAGGGTGGACTG AAGATCTGTTGGCAGGGCTCAGAGACGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAG/A/GJTCCTCCAATTTTCAGGGGCTCCC GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCAATGTGTCTGTCTCATCCAATAAGCAGT/GJ/CATGACCTCAGCCCCACTCTTTCTCCC TATGTTCCAGAGACAGAATAGACCTGGCCCCCTTCCCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAATAAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTCGTTAACTGTGTATGACATA TATATATTTTAAATTTGATT/GJAAAGCTGATTACTGTCAATAACAGCTTCATGCCCTTTGTAAAGTT ATTTCTGTTGTTGTTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTATAAAGTATATAATTTTTTATGTTTGTCTGA

WI-7747a	44	T C ---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCCTGC/TCTTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTTCATGCTTTTGTAAGTT ATTTCTGTTGTTGTTGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAGTATATAATTTTCTGTTTCTCTGA
WI-7189	197	T C ---	---	TCAGAAATTTCTCTCAGCTCATTTTGTCTCTCACAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCAATTAATTTCCCTTCAAACAATAATATTTACAGAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAACATTTTTC/CJAG TTTGCAATAGAACTAATACTGGTGAAAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---	---	AGCCCCAGCTGGACTCATGGATGTCACCCCTTGTCCCTGCTCTTCTGCCTCG/GA/CJTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCCTGCTGAAGCT GAGAAGGCACAGGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCCTCATTT ATTGGTGAATGATGAATGGGAATGAATCAGGGGGCTGCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTCTCTTATCCCATCAACCCCTAAATAGGTCAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G/GC/JAGAAGTGAAGGAAGATAGGAAGATATACCTCTCTGTTATTTTAAAGAACATTTGTT GGTGGCAGCAATCTCCCTGTCCTATCACTGTAGAGGCCAATTTATATCTATAAATATATATAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATATTTGTCAAAAGTTTAAAT
WI-7919	242	T C ---	---	GAAGGCAGCTGGATCACTTCCCGCAGTCCCTGGGCAGCGCTTGTGTGGAACACAGAGAGCTCCTCT CAGGGGCCCTGGCAGCTCAGCTCACTTCTATTCTGTATGATGATTTGGTTAAACACTGTCAAATAAGAGAT GTGCCAGATTTAGATTTTCTACCCCTAATCTGTGTTAATATTGTAACCTTTATCCATTTGAAAGTGCA AGCCCATTTCAGATAAGCTATAATCTGGTCTTTAAGGAA/TTC/JACAACCTT
WI-7928	101	T G ---	---	CTCCCTCCTATGCTCTCAGCAGCAGCTGGGGCACACTTGTTCATCTCTGACCGTTTGTGGGCTA TTCCCTCGAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAAAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAAGACTTAAAGGGGCCAATGAATTAATATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTTCTTTGGAGTTAAATGCAATATAGACACATACACCCAAACACTTACACCAAAC(T/A) ACTGAATGAAGAAGTATTTGGTAACCAAGGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAACAAAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACAGTTCCAGCCGTTGCCCACTCATCTGCGGCTTGTCTTGGTGGGGGCAGATTGGGTGG AATGCTTCCATCTCCAGGAGACTTTCATG/TJAGCCCCAAAGTACAGCCTGGACCAACCCCTGGTGTG TGTAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCCTGAGCCATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	TTTCTAGGCTGACAGCTGATGCATGATTTTTTATAAATATTTTATCATCTCTGTGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTA/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTCAATGTGGAATAGTTTAAACAGTCAGGAAGGCTAAACTGGTCACTAATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	GGCCAGGAGATTAGCAACAGGATCTTCTGTACTTACTTGGCCCTTTTATCTTCCCTCTTGGCC CAGTCCCTTCTCTCCAGTTCTGGAAGCTCTGCACAGACAGACACTCAGTGTCTTGGCAGTGCT [G/T]TACTCTCTCAGGTGCAGCATACATAACCAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAAAATGTCATCAG
WI-140	252 C T ---	---	ATTTGAAGATTGGAGGGCTTTCAGAGGAAAATAGATTTCATTTGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTACCAGTAAAGTTTATA TCTCCATTGAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTTAGTTTAAAAATGTGTCATTTGCTGTATTGGCAATTCCT[C/
WI-198	218 C T ---	---	GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCAAC CATGATGGAACCTCTTGCCATGGTTTAGTACCCTGGACCAAGTAGTCAATCCCTGACTTTAAAA TCTAAACAGCCTTTGATGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTACGCTA CCTGCTCCCTTTC[C/T]GTTTAAACAAGCATAGAATATCTGAACAAC
WI-205c	146 T C ---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCTAACTATGACTTGGTCGG AAGCCAAGAACCCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTG[C/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCTAACTATGACTTGGTCGG AAGCCAAGAACCCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTG[C/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	GAAGACTGAGTTTCCAGAGGTTGCAGCCGTTTCTCTCGGGCCCATATGGCTAATAAGGAGCTTGAGCA GGGATTTCAACCTGTTTGCACCCCAAGTNCCTTCCAAGAGGTCTCAGACTACCTCTCCATCTCCCCCT CTCCCCACACACACAAAATACAGAGATTG/CJAATTCAGGAGCCAGTTTCTAGGTGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTAGTTTCTCAAAATGGGAATGG
WI-276b	25 A G ---	---	AGCTTTGAAATCCAAAACCACATGAGTCTTATCTCTCTTATCTCTCTTGTGTAACTATCTATCC CTGAGGCAGAAAATACAGAACACCTCTGGCTGCTGACCGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCTCTCTGCTATCTCTGATGACTGGGCAAA

WI-276	25 A G ---	---	AGCTTTTGAATCCAAACCACATG/GJCTTGACTCTCTTATCCTCCTCTGTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCCTGAAAGACCCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTATCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	TTTTCCCAATCCACAGTAAACATAATAATGGATATAGAAATTTAGAACTACTTCC[G/A]GTTT TTTCCCTGGGAAAATATTCACAAACATTTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCCTGACTCTGGCAGGATAGTACCAGTCTGTGAGACTTTATGT ATTCATTATTAGAGCCAGGGTCTTGCTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAAT/CJAAATGGTCCTTTTTAAATAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAAT/CJAAATGGTCCTTTTTAAATAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAAT/CJAAATGGTCCTTTTTAAATAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT/A/GJCATGATAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---	---	TTCAAAATTTAACACCATGGGTATATTAAATTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGTCCTTGACGTATTAACTGATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCTCACCCTAGTTGGCTCTGACTTCTTCTTCTGCTGGCT GAACCTTCTCTGTGTGGCTGTCGGCTTCTCTGCTGCTGGCTTCCAAATAC
WI-681b	156 A G ---	---	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACATATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGTTT
WI-681	156 A G ---	---	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACATATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGTTT
WI-867b	119 G A ---	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTGTGTGTTTGGC CAAATAATCTCCCCAGGACGTCCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCTCCCAACAAAGCACACATTAGAAACTTA
WI-867	113 A G ---	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTGTGTGTTTGGC CAAATAATCTCCCCAGGACGTCCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCTCCCAACAAAGCACACATTAGAAACTTA
WI-867	119 G A ---	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTGTGTGTTTGGC CAAATAATCTCCCCAGGACGTCCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCTCCCAACAAAGCACACATTAGAAACTTA
WI-871b	123 C G ---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGACACTGTTATGGCTGAAATGTTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATTTGTACATAA
WI-871	123 C G ---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGACACTGTTATGGCTGAAATGTTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATTTGTACATAA

WI-884	198	T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTTGGTNGTGGAGAAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGTATCTAGTCCATCCCTTTATTAGGAACCTTCTCGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCCGCATGCAACATTTTATTCAGTGAACATGATGAAATGAACATAAT
WI-921b	205	G A ---	---	CACATCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCAGCCCTGGCCCCCAAGAAAGTCTNGCCAGGAAAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-921	205	G A ---	---	CACATCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCAGCCCTGGCCCCCAAGAAAGTCTNGCCAGGAAAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-945c	90	G C ---	---	GGCTGGGATGAGAGGTTCTACTTGTGTTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNNGGTT TTCTCTGGTCATAGAAATCTCTTAAAGGGAAATCATGACAGATTTCTTGGCTTTA
WI-945b	90	G C ---	---	GGCTGGGATGAGAGGTTCTACTTGTGTTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNNGGTT TTCTCTGGTCATAGAAATCTCTTAAAGGGAAATCATGACAGATTTCTTGGCTTTA
WI-960b	167	C T ---	---	TTGCTTCAAGAAGTTCTTGTCTCAGGAAGTTATTCATTTCAGCAACCTAAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A ---	---	TTGCTTCAAGAAGTTCTTGTCTCAGGAAGTTATTCATTTCAGCAACCTAAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATG/AJTAAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C ---	---	TCCCAGTGTAGTATGGCTTTCAGTAGTTTATTATGATGCGCTAGGTACATTTGTTTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTCTGACCCCTTTCTGTGTTTC CTTCTTAAAGATACAAAATAAATGTAAACATTAGACCTCTCAGTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATGCTCIGGCTTCATTTTGTAAATNG

WI-1147b	204 G A ---	---	---	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGCTCCAGGGTTTTCACAGGATTAGTGGTCAGTCA CATAGGCATATAGTACCTGATCTCTATCCAGCCACGCAAACTTCTCCTCCCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACTTTGTAGGATGAACCTATCTGGCCAAACTGATA CIGAGCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 C T ---	---	---	GCATTGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATCGCCAGGTGGC TAAGTGTGGGGC/TTCTGGGGTCAGGCTGCCTGGGTGCATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---	---	---	GCATTGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATGIC/GGCCAGGT GGCTAAGTGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTGCATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---	---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATGN/TCIGNCANT AAAAATGATTGAAATTGGGAATAAGCCCTCCCTCTAATGATTGACAGTGTAGACCTTGCCTAG GAC
WI-1305d	202 C T ---	---	---	TTCTCAATCCAACTGCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTCCCTACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNATATG[C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 C T ---	---	---	TTCTCAATTCCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCT/TTATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTCCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 T C ---	---	---	TTCTCAATTCCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTCCCTACA TCCACTGCTTTCANTAAAT/CTJNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 C T ---	---	---	TTCTCAATTCCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTCCCTACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNATATG[C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	TTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGTGACTGTCCTGGTCAATTTAGAGCCATAGAGTGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGACCTAAGGNGAGAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGCCAGTTGAAATTTATCTTCTT[A/G]G[C]
WI-1306	240 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGTGACTGTCCTGGTCAATTTAGAGCCATAGAGTGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGACCTAAGGNGAGAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGCCAGTTGAAATTT[A/G]TCTTCTAGC
WI-1307b	118 T C ---	---	GACAAGGCTGGTACTAGTTTCCAATTCCTCAATCTATGTACACTTCTCCTCACTTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGCTTT CCTACCTCTTAATGTATCTTNCATTAATATGCTAAACCGGTACTGTGATCTATCACTGGTT TCITTTGGTGTTGTTGTTGCTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118 T C ---	---	GACAAGGCTGGTACTAGTTTCCAATTCCTCAATCTATGTACACTTCTCCTCACTTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGCTTT CCTACCTCTTAATGTATCTTNCATTAATATGCTAAACCGGTACTGTGATCTATCACTGGTT TCITTTGGTGTTGTTGTTGCTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169 T C ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCTCT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCTCT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGATGCAAGAAGTCTGTTATTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGTACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGATGCAAGAAGTCTGTTATTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGT/CJGTACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCATCTCTAAG

WI-1341b	136 G A ---	---	TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTGNTGCNNNTCCCTTTTCNTTT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAAATTTGGCTTCTTGTNAATATACCCAAGC [G]AGGATTGGATGCTGTTTATTTCTGTGCTTGGACAGCAGAGTCTCTGNGAGTNG GTTTCAGGATTGCTCTGTTTCCCGAGCCACTTGCACATTAGCAAGTGT
WI-1349e	192 GC ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349d	264 C A ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTGAGAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349c	192 GC ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349b	264 C A ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTGAGAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349	264 C A ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTGAGAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1403b	57 CT ---	---	TGGTATTTGGAATGGGTTCCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]CCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTTCTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58 T C ---	---	TGGTATTTGGAATGGGTTCCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]CCGA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTTCTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1417c	31 C T ---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGCCAGGGCGGCAGATGTGAGCCACGGG GGTGACAGCATGCCCTGCTGGCATTGGAGGGCCOCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGAGCGCGTTGC AGGCGAGGCCCTTAGGTCGGTATTAAATGTTTGTCTTTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGCCAGGGCGGCAGATGTGAGCCACGGG GGTGACAGCATGCCCTGCTGGCATTGGAGGGCCOCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGAGCGCGTTGC AGGCGAGGCCCTTAGGTCGGTATTAAATGTTTGTCTTTAGAAAAAGTCGC
WI-1729	172 A ---	---	CCATGAGCAACAGCATGTTCTACTCTGTGATGTATGTTAGGGGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGTATGTGCTCTCCGTGGTNAOCTTCTCTCCACCACATCACTGTGTTTTT
WI-1732b	122 T C ---	---	TGCCTACTTCTTTGTTCAATCCACCATTACATTTGTAAATTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTTCATTCACTCT CTGCCACATGCTAGTAACGTGTAGTGATGGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCAATCATATGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1732	114 C T ---	---	TGCCTACTTCTTTGTTCAATCCACCATTACATTTGTAAATTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTTCATTCACTCT CTGCCACATGCTAGTAACGTGTAGTGATGGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCAATCATATGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAAGGTAGTAATTCCTTTCCCCCAAAAAGGTTTAAAACTGTGTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGAG/GJTTAAGGTGTGCTGTTTCTGGCAAAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAAACCGGCTTGCACTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAAATCTAC/GJTAGCGCCTTAACATTTGGCTGAGTATTAATC TGTACATGTGTATGTGAACCCACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAAGTACAATTAC TGGGAACTGTAGAACAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAAGAAATAATCATAAAAAT
WI-1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/GJAGTAGGGTAGAGCATCACACTTGGGAGGACATATTCGGAGTNAATATCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTAATCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA

WI-1803b	77 A G ---			CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATAGTAGGTAGGTAGAGCATACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATACATTACTCTTGCTCCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---			TTTACTTGGGATTTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/TTCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGGAACGTTTTCAGCTTCTGCTGGCT
WI-1837	112 C T ---			TTTACTTGGGATTTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/TTCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGGAACGTTTTCAGCTTCTGCTGGCT
WI-1840b	79 G T ---			TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TTGAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAGTTCTTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---			TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TTGAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAGTTCTTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T ---			GGGCTCACTTTCATCAGAGCACATATCACGTGATAGTGTCTCTCTTTTCATAACTACTCCCGG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/TTGCTGCAAAATAAACTCCCAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTTGTTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---			GGGCTCACTTTCATCAGAGCACATATCACGTGATAGTGTCTCTCTTTTCATAACTACTCCCGG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/TTGCTGCAAAATAAACTCCCAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTTGTTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---			TGTTCTCTGCTCCAGGCACCGGCTAAGTCTTTGCTGCTGATAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGCT/TTGCTCTGAGAGGT AAAGTCCCTGCCCAACGCGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCGCT GACTTCAGATCTGTGTCTTAACTGCCATGAGAAAACCACTTTCTTTTGCTCC

WI-1900	119	C T	---	---	TGTTCTGCTGGTCCAGGCCCGGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAAACCCNG CTNAGGTAGNNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGG[C/][G]CTCTGAGAGGT AAAGTGCCCTGCCCAACCGGCACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGIGTCTTAACCTGCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165	C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGAACCCAGCC[C/][T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA AGCAAGCCAATGGTAGGGAAGAACCCAGCC[C/][T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165	C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGAACCCAGCC[C/][T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164	C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGAACCCAGCC[C/][T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270	A T	---	---	CCAGGTGAGGCTGAAAGAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCAACCTCCCAACTTT
WI-1960b	270	A T	---	---	CCAGGTGAGGCTGAAAGAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCAACCTCCCAACTTT
WI-1977	203	T C	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTCTCATAGAGTNTGTTTTTAGTCTCGTAATAACTGTTGGCCCTAGGAAGGTTGTT TTCTCTACTGGCTGTGAAAGCCCTTCCCATCGAGTGATACAGTACTTTCAGATTATGGAGATTTT /CTAACAAATCAACACTGGCTGAGGCTGTTGG
WI-2012	102	T C	---	---	AAATCTAGAAGCCAGAGTCAGCTCAGGATTTATAAGTTGAAGTAATGCATTGTAGTTTCATGT TTCTCTTAAATCTGCACAAACTAGCTAAAAATC[T/][C]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGTGTCTCTGAGTCACTTTTTTCTACTCTCAT GGCTTCACCAATGCTTCCACTGGATC

WI-2013	127 C T ...	---	CTTTAGAGGTGGTCATTCGGTCCCTTCTGGAAAGTGATTCGGTGTAAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCTACGCTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A ...	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACG/AJTGTTGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTTGGTTAGGCTCACCTTCCCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2032b	219 C G ...	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACG/TGTTGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA/C/GCTTCTCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2032	219 C G ...	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACG/TGTTGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA/C/GCTTCTCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2054b	188 C T ...	---	CGTTTCTTCTACATCTTGGGNNACATAAAGANGAAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCT/C/GTTCCTCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2054	183 T C ...	---	CGTTTCTTCTACATCTTGGGNNACATAAAGANGAAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCT/C/GTTCCTCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2573d	129 T C ...	---	TGGGATTAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACTTGCCGTTCAAGGTTTCCGTCGTTT/CJ/GA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCTAGGTAGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAAGGTCATATGGCTGGCTTGGACGAG
WI-2573c	165 A C ...	---	TGGGATTAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACTTGCCGTTCAAGGTTTCCGTCGTTTGTGATAT CATCTGATCTTCCCAACCAGGGCTTATTT/CJ/GCTAGGTAGGGTAAAGCAACAGAGGCTGTGT TGAAGTGAATGATTTGCTTGCACAAGGTCATATGGCTGGCTTGGACGAG

WI-2954c	49 T A ---	---	---	TTAGCACATATCTGTTGGGACTTAAGTGAACAAGGCATAAAAAAT/AJ/CAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	---	TTAGCACATATCTGTTGGGACTTAAGTGAACAAGGCATAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	---	TTAGCACATATCTGTTGGGACTTAAGTGAACAAGGCATAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTCCAGTTAGACTACCCAGCATTTCTAAGAAT/CJG CTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTGTAACTCCTCCTCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAAACCTTTTACTTAGGATTGTCT
WI-2971	62 T C ---	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTCCAGTTAGACTACCCAGCATTTCTAAGAAT/CJG CTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTGTAACTCCTCCTCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAAACCTTTTACTTAGGATTGTCT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTAA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTAA AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTAA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133 A T ---	---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCCAGCTTGAGACAC ATCTCAGTTAGCTCCTT[C/C]CTGCGCATATCCTGTTTCTTCTTACTCCTATCTCCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCTCAGTCTGCTTTNAGGGAACITTGACCTAAGACAGAA ATCTTAGTACCAATACITTTGCAAGG
WI-3147	85 C T ---	---	---	ATTCTGTAATGTTTTCAGTCTCCAGTAAATTCITTTATTGAGGTCCATGTCCATTACCTTACTTA T/C]GACAAGCAAGAACAAACAGAAAGCCCTCTGTTTGGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATATCATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTNATACTTAT
WI-3234b	68 T C ---	---	---	ATTCTGTAATGTTTTCAGTCTCCAGTAAATTCITTTATTGAGGTCCATGTCCATTACCTTACTTA T/C]GACAAGCAAGAACAAACAGAAAGCCCTCTGTTTGGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATATCATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTNATACTTAT
WI-3234	68 T C ---	---	---	TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTNATACTTAT

WI-3292b	106 G A ---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[GA]TGGATTGGATGGGATGATTCTT GCCATGAATATTTCCATTGTTCTCATTAATGATTAATTAATTAAGTAAATATATTNCCATGA GACACAATGGAAAAATGGAACATTCATGGAAAAAACCCATTCCAATC
WI-3292	106 G A ---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[GA]TGGATTGGATGGGATGATTCTT GCCATGAATATTTCCATTGTTCTCATTAATGATTAATTAATTAAGTAAATATATTNCCATGA GACACAATGGAAAAATGGAACATTCATGGAAAAAACCCATTCCAATC
WI-3355	19 G C ---	---	---	CCATGAACCATGGGTACA[G/C]ATATTCTTAACITTCAGAGTCCCTCTTACTGGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATATACTTCCCTCCAAGCACCTTAAACATCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194 G A ---	---	---	CCATGAAGAATGAGTTCTCCCTCCCTGGGTACGTCAGTCTAAGAATAGCACACCCCTTGAGAAATTNACT TAGCACGTGGCATTGTAATGGCTGGATTCTCCGCTCTAAGACACACCTTTATGCTTTTCAAGCTTT CTGGAATTGGGATGAATCNACATCAATGTGCACCCCTCGTGGGATCATTCTCC[GA]TGCCTCC ATCTCTGGNAGAAAGCCACTGGGAAGTCGAAGGAGTCAATCAATCAGG
WI-3505b	131 G A ---	---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTTGTGCATCAGTGCACCTTAAAAAATTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCCCTAACACATTAACCTATTTTNAACCAAAC[GA] AGGTGATTCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAAATATGTTGCATAT
WI-3505	131 G A ---	---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTTGTGCATCAGTGCACCTTAAAAAATTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCCCTAACACATTAACCTATTTTNAACCAAAC[GA] AGGTGATTCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAAATATGTTGCATAT
WI-3564b	177 C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTCCCAAGTCAGGAGAGTCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGTCTCCAGTGTATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTGGTGAACGTTAACATGCTGTCTGT[CT]AACAAAGTGTGTTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTTCAAAAAACAAA
WI-3564	177 C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTCCCAAGTCAGGAGAGTCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGTCTCCAGTGTATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTGGTGAACGTTAACATGCTGTCTGT[CT]AACAAAGTGTGTTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTTCAAAAAACAAA

WI-4110	130	T C ---	---	GAAAAATGATGTTTGAATTCCTTCCTATCTTCAGATTATGGAGTGTCTATAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCTCTTCCTGCTTTATTTTGCC[T/C]ACA GTTTAGGTAAATAAAGATGCCAAGAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAGGAGGAGGTTGGGGGTTTCTGGGAAGA
WI-4119b	168	GA ---	---	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTCA TGAGACCGTCTGCATTCTTTGTTTTTAAAGGGCTCTGTGATCATCATCTTCA
WI-4119	168	GA ---	---	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTCA TGAGACCGTCTGCATTCTTTGTTTTTAAAGGGCTCTGTGATCATCATCTTCA
WI-4123b	51	T G ---	---	CAAAGTCAGATTTGATTATTCAGGATAACAAATTTTGAATAAGAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAATTTGATAGAATTTAGTGGG TTCTCCATGACATTGGCTTCTTCTCAACAGTGGGTGGTGGATGTTTCTTAAGCTTTCTC AGGCACAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G ---	---	CAAAGTCAGATTTGATTATTCAGGATAACAAATTTTGAATAAGAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAATTTGATAGAATTTAGTGGG TTCTCCATGACATTGGCTTCTTCTCAACAGTGGGTGGTGGATGTTTCTTAAGCTTTCTC AGGCACAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	GC ---	---	TTGTACATGTTTCATTCCTCCCTCCCATCTTTCTGCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAGCTTTCTCAGCATCTCTATATACT GTGCTGT[G/C]CCTTGGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTAACCTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---	---	TTGTACATGTTTCATTCCTCCCTCCCATCTTTCTGCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAGCTTTCTCAGCATCTCTATATACT T/C]GTGCTGTGCTTGGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTAACCTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188	GA ---	---	TAACACACTTTTCATTTGGTTTCTTACTGCGAGTTAAAGGACCATCCATTATATACAATCCCTC AGTTCTATGCTTTAGAGTNCATTTATAGGACTACTGTAATAATTCAGAGGGAATTAAGCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTTGCAGGGGACTGTGGTTAA[G/A]ATGCTCTCT TGCCCCCTTCCCAAGTTCTTAAATTCCTAG

WI-4230	93	T	---	---	AGAGACGTTGAATGGGGACATCTTTTCATTTTCGATTTTAGTTTAACTTTGATAAGAATTGATGAAA GTTTGTACATTCAGATTATCTTTATAGCAGCAGAAGCTGGCAATAAATACAGCACACTGACT TTTCCATGGTAAAAAGAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGGAGAATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118	C	T	---	GAAAAATCCATTGAAGTTTGACCTTGAACCTGATCTCATTAATACCTTTTNCCTGTAGTGGTTGATTT CATTTTGGACAACAGACAGAGCAAAATTTCCACTTAAATTAATTTCTC/C/TJAGATATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTAATCTCTAGATATCTCTCAGAAATCTAGGATGGAAG AA
WI-4271b	151	A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTGAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTACAGGGAGCCCCAACCCCTCCCTTTGTCTCAGG CTCTAGAAAGTCCAGTCAGGGGC
WI-4271	151	A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTGAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTACAGGGAGCCCCAACCCCTCCCTTTGTCTCAGG CTCTAGAAAGTCCAGTCAGGGGC
WI-4389b	156	G	A	---	AATCGAAACATTGATTTTGTAAAGGAACCACTATTATGATATTTGTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156	G	A	---	AATCGAAACATTGATTTTGTAAAGGAACCACTATTATGATATTTGTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31	A	G	---	GATGACAATTATTGTGATTGGCATTTTAA[A/G]GTACCATTCCATTTCTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTAGTCGATTGCTCCTTTTCTAGTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCTCAAACTGATCTTTAAGAACAATAAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145	G	C	---	ACCATCAATGTATCACCTTCTAAAAATTTATTAGATGATTAACTGGCTCTGTAAAAATAAAAAACCT GTCTTGGACATTGAAAAATAAACATTAATGTTGCTATTTCTGCTACTTACAAAGGTACTGCACTA AACAAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACCTGTCA TTCTTGCCCCATAAATAAAATTTTACATGCTT

WI-4584	144	A G ---	---	TTGGTTGGCA TTTAGCCTCATAACAAC TATTACAATCATAA TGTACTCTTATTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCAGGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGTAAAAAATGTTTAAATCTATGGCATTAGATTTCAAAGA GTCTAATGTGGTTTGAAATAGGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185	C T ---	---	TTTCTGCATTGAATGTTGATGTCAGACTTCAGAGGAACCCAGGAATCTCATTTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAATCCACCAATTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTTGTA AATTTAAGGACACCTCATCATAGTAATTTGTGAGGATAAAATGAAATAA
WI-5327	63	A ---	---	AAATGAATCGGCTTTAGAGCAAATACCAGTAAGGCTGGTGCGAGGATGGTGGCTGAGAGA[A/-] JGATTACTCATAAAAGCATATTAAATTTTATAAATATGGAATAATTAAC TAGATAAATTAATGTGAAT TGAGTTTGAAGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGATGGCTCTTCGGATGACATGATGAATGTTCTTAAGCAGACAG
WI-5390	87	C T ---	---	GCTTTGAGAAATGAAAGGGGAGCCTGGACCATTGCAGGGCTCTTCATCTCTGATTATTTTGTGTAT TTATTGTTCACTTATTTAT[C/T]GCTGCTCCCTTCTGCTGATGCTTGTGTCATGAACAATGAATTC CCAGTGCCTGGCCGATTCGTGGCTCCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAATTG ACGAATGGTTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATATTTTAAATTT[G/A]AAAGAAACTTGTTTCTGAAACTTTGTAATCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAAGGTTTATAGAGTTCAACAA
WI-5404	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATATTTTAAATTT[G/A]AAAGAAACTTGTTTCTGAAACTTTGTAATCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAAGGTTTATAGAGTTCAACAA
WI-5545b	77	A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTCACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTTC
WI-5545	77	A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTCACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTTC

WI-5860b	134	A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAAATTATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACACAC GJTATACGGAATCATGTGAAGACATTCTAAAGGGTACCAGGTGCACATAGTTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAAATTATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACACAC GJTATACGGAATCATGTGAAGACATTCTAAAGGGTACCAGGTGCACATAGTTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	GCAAAACACCTATTATACCTGATTCACACCCAGGTCTACTAACATTAAATCAACCCTAACCACAATAC TATATATTGTCCTGTTCTGAATTTATTTCAITTAGAATCTGATGAGATTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTTCTACAGAG TAATTTCGJATAGTAGGTACCCACCAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTC AAACCTATATTNCTGCTTGTGTCATCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109c	147	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTAA ACCCTATATTNCTGTCCTGTCATCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109b	147	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTC ACCCTATATTNCTGTCCTGTCATCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109a	129	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTC AAACCTATATTNCTGTCCTGTCATCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6112	96	T C ---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTTGTTCAATGATTCGTCATATCCCAAGTGCCTTAGACAATGCTCCCATAC AGTGAACAGATTTTGACTAAACACATACTTGTAAATCAATAAAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103	T C	---	---	TAATTGCACAACCTTACATATCAGGGTTTCTGATTGAAAGGAAGAATAATTCTCTTTTAGTGATT GCTTAATATTAAATTCATAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACCAAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTCTTCTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T	---	---	CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCCTAGTAGGGCTTTGGGTGTGGCACCGTTTGGCTCATTCTCTACTCCCT GGGTCTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAACCTGCTTCTTTCGAGAAAGAGTCG GGTTCCAAAGATTTCGTACGATTTTITA
WI-6336b	234	C T	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTCTGAGGACACTGACAGT
WI-6336	234	C T	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTCTGAGGACACTGACAGT
WI-6381	92	C A	---	---	TTGGATACAAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTAAACA[C/A]GTATTTTAAAGCTCAAAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCCACCATGGGCTTTTGAATGTCTCTCACTCCCAACTTCACAATCAAAATC TACAGANGGGCAAAAGATCAGAGTTTCAG
WI-6436	198	C G	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCTATAATAAGAAGTTAGACTTTGGGTGTAGTAGTTGATAGTAGTAGGAGCGTT[C/ G]ATTGGGTGATTCACACAGACAGGTGATGTTCTAAGATTGATATTTATTGT
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTGGTGTCTCAGACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTATCATCTGCAATCTCTGATCTTATGCTGGCTCTATT[C/AT]CCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCTCTAATTTTCTGIGGGIATTATA
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTGGTGTCTCAGACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTATCATCTGCAATCTCTGATCTTATGCTGGCTCTATT[C/AT]CCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCTCTAATTTTCTGIGGGIATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAGACCTCCAAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACAATTCGTGAAAAAATTAAGTAGAACTCAAGAGGCCAAAAGTCCCAATTTGTGTCCATTA TAAGAAATATTTGAATGGAATCTTAAGAATGATTTTATGATCAGTTAAATGTTCTTCTCCTCCTC CAGTCCCATTTATGACATCCGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAATCTTCCATCGCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAATCTTCCATCGCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACTCAATTAACCTTTCACAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTATTTTGTGA CACTGTCTATTTACCTCCCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACTCAATTAACCTTTCACAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTATTTTGTGA CACTGTCTATTTACCTCCCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAAATTTTAAAAAGAGAACAGGAAATAGGAAGGCCCTAACAGAGGAG TTAAATAATTTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATGGTCTACCAATGTGACTCTTTACCCAGGCCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTCGTGAATAATCTCAATTAATTTCTCCTNCCCTATTCCTTTCCAT GCTCGCTCATTTNCTCAGAAATGGAAGGCATTTGATTATNATTTTTTTGTTGGGTCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATGGTCTACCAATGTGACTCTTTACCCAGGCCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTCGTGAATAATCTCAATTAATTTCTCCTNCCCTATTCCTTTCCAT GCTCGCTCATTTNCTCAGAAATGGAAGGCATTTGATTATNATTTTTTTGTTGGGTCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA

WI-6608b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAGAAAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAGAAAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6666	68 CA	---	---	GTTAGACAGTATCCAGCAAAAAGGTTATTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCCC AIC/AJAAATCCCATCAACACACAGTCATGCTGGAAGGCATTCGTCTTACTCTGTGGTTTCATGTAA ATGTTGGGTGACTCATTCGGCTCTCTNTTCTCAAGTCCAGGCTCTTGGGTAGACCAAAACTA ATACAAATGTTAGACACACAAGAGA
WI-6670b	120 A	G	---	AGATTACATAATTATCTAGGGCCCATGTAGGGTTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTTAGCCA GCATTGCCATTGAGGGCCGGAGTCAGGGTTTGTGGGCCAGAGTTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTTGTAACACACAGACACAGAACTCTTAGAAGGGAT
WI-6670	120 A	G	---	AGATTACATAATTATCTAGGGCCCATGTAGGGTTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTTAGCCA GCATTGCCATTGAGGGCCGGAGTCAGGGTTTGTGGGCCAGAGTTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTTGTAACACACAGACACAGAACTCTTAGAAGGGAT
WI-6704c	33 T	C	---	TTTGAAAATAAATTATGCACCAATGTTTAACT/CJACACATATATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T	C	---	TTTGAAAATAAATTATGCACCAATGTTTAACT/CJACACATATATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T	C	---	TTTGAAAATAAATTATGCACCAATGTTTAACT/CJAACTCACATATATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---	---	---	CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGTAATACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACACATTTTGTAGGCTGGAATGATTCCC[G]ATAGTAAACCTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTATTAAGTGTGACACAGGATGTACCCAGTGAGCCTC ATCCAGTCCAAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGTC
WI-6766b	148 G C ---	---	---	AAACAAATGGTGCAATTCGATAATTTGGTGCACAGTATAAAACAATACAATTAGTTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]CJAAAGTCAACGTTTCTCTTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCAAATCCCAGTTCCTCTTC
WI-6766	148 G C ---	---	---	AAACAAATGGTGCAATTCGATAATTTGGTGCACAGTATAAAACAATACAATTAGTTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]CJAAAGTCAACGTTTCTCTTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCAAATCCCAGTTCCTCTTC
WI-6787b	97 A G ---	---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTACAGACTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAATTTCAAC[G]ATTTTACTGCATAAGATATCTTCATGTACAACGTG ATGCTTTGTCTTCTTGGGAAGGACGCTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	---	GAACCCACAGGTCCTGTTATTTTATTAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAGGGCGGCTTCAAATCAATCAATCAGTCAACCCCTC[G]GAGTTAGAAAGTAGAGTCAAGGAA GAGCTGCTGGCTGTAGGAAGTAGGGTTAATGCCCTTAATCCCTTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACAGTTTCTCATCACAGGTAAAGGCAAC
WI-6810b	37 T C ---	---	---	CACAATAATAAATCACTCCCTACCTACCTTGAACCTTTAT/CJAGAAGCATTTTTAATTTTACAACACA AAGCTCAACGNACTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTAAATGTCTATGNACAAGTACAATTTCTTTTGTAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	---	CACAATAATAAATCACTCCCTACCTACCTTGAACCTTTAT/CJAGAAGCATTTTTAATTTTACAACACA AAGCTCAACGNACTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTAAATGTCTATGNACAAGTACAATTTCTTTTGTAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	---	GCATGATTAAACCAGTGCAGAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTCTAGTA TTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAACATCACTAATCACTCAACAATGTAGCT GCAGGGTAAAC[C]A/JGTGGATACCCCTGTGTGCTCTACTINGCCCTCCAAAGGCATCAGGGGATCATCA AAGATGTTGGACACCTTGTGTCAATCTTGGTTACAGTGGGCTGTGCAG

WI-6817	145 C A ---				GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGTAAAC[C]ATGTGGATACCTGTGTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTGTGTCAAACTTGGTTCAGGTGCGGCTGTGCAG
WI-6819b	221 C ---				GATGGAAGGCCATTTATTTCTCTAAATTTAAATAGAAGACTTTAATGGAACATTTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTG CTTAGCAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCAG
WI-6819a	175 G T ---				GATGGAAGGCCATTTATTTCTCTAAATTTAAATAGAAGACTTTAATGGAACATTTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTT TTGCTTAGCAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATAT
WI-6826b	154 A G ---				GCAAAAAGCTTTATTGGCTCCAAATAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTGACAT[G]GAGCTTAAATAATCAAAATGCAATATAGATTGGGTGCACGTG TAAGCTGAATTGCAATATATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154 A G ---				GCAAAAAGCTTTATTGGCTCCAAATAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTGACAT[G]GAGCTTAAATAATCAAAATGCAATATAGATTGGGTGCACGTG TAAGCTGAATTGCAATATATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122 T C ---				AGTGCAAACTATTTGAAACAAAGTAACTATGAGTCACAGCATTGAGCAAGACATCAGACACGGA AGAGTGAACATATTCCTAAGTAAATACAGCAGATGAGATGCTCTCACATGT[C]JATTTAAT TATTCATGCTTTTCAATAGTCTTTAGTCAACTTTGAGTGAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153 G A ---				TTATAGAATACTTATGGGGCATACNGTAAATGAACCTGCAACCTTAAATCTAAACAACAGCTTG TTTGTTGGTTCCTGAAATCCTCCCTGCTCACAACACAGCCAGCTACTNGGTTTCTAAAAGACGTA ATTTGCAGGCAACTTC[G]ATGAGGCCATTCCTGTGCAAGAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGCTGTGTAGAACTGAGCTCAATTA
WI-6909	73 C T ---				ATTGAAAACCTGGTAGCAACAGATAAATACAATAGAGCCTGGATATAAAATGAGAGAAGATGC AGACTT[C]TJAAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCTTTTTGGCAACAGGATTATTCGAATAATAATCTGCCAGTGCCCAATCAG AACACCATTTCCACAATATTTGCAIGCCCCCTAGTTGCCCTATTTTATACATAIC

WI-6910b	163	G T ...	---	---	CACTCAAAACCTTTATTGATTGATTTACAAACGTGACAAATATTTACAAAGTTTAGGCATTATCCCA TATTGACATGAATGCTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/JTGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A ...	---	---	GCTTGTTTTTTTGTTTTTAAAGTGACACCTTGGCTTGCGGCTTTCTTCACTTATCTTACCC AAAAGTGCTTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGTGAATTCAGGTGATTTNATTTTCTATTGGTAGTATTTTCAGATTTCCCAAAAGAACATG TATTGCTTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T C ...	---	---	CAATCAAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAGGGGTGAGCTAAAGGTCJAAGTCTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C ...	---	---	CAATCAAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAGGGGTGAGCTAAAGGTCJAAGTCTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A ...	---	---	TTTTATGAAACATTTGAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAATTCCTAGTAAAGTAAAGTATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATAANCAAAATGNGTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAGC
WI-6955	79	G A ...	---	---	TTTTATGAAACATTTGAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAATTCCTAGTAAAGTAAAGTATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATAANCAAAATGNGTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAGC
WI-6957	47	C G ...	---	---	AAACTAAAAACCCCTTATTGTCTCCAAAGTGTGGCAAAATAGAAAAT[G/JTTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCACCTTAAGAAAGCATTCAGTCAAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAACTGGATTTGAAAACCACTTTAGG CTAAAATAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242	G T ...	---	---	ACTTCTAGTGCCTCTGTACCACACCTCTAATGCCCTCTGGTCCCGCACTTCTGTATGCCGTAGGCCCT TAAATCTGCCTGGGTCCCTCCCTCTGTCTTCAGACCCAGAGGAGAGCCGCGCAGTTCCCTG CAGGAGAGAGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGAACCCCTGCTCCTGACT CTCTCTGATGGTGGGCCCTCTGTGCTCTTCTCTCTCC[G/JTGICGGATC

WI-6996b	242	G T	---			ACTCTAGTGCCTCTGTTACCAACCACTCTAATGCCCTCTGTGTCGCCGCACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGTCTTCCAGCACCCAGAGGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCTGCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCCGCTGCTCGGATC
WI-6996	228	T G	---			ACTTCTAGTGCCTCTGTTACCAACCACTCTAATGCCCTCTGTGTCGCCGCACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGTCTTCCAGCACCCAGAGGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCTGCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCCGTCGGATC
WI-7021b	112	G A	---			TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTCT CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAATGAGTCCCAAATGAGTCCCAAATGAGT CTTCAGCTCTCTTGACATCAAGGCTCTTCGGTCCACATCCACAGACCAATCCAAATTAATCAAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---			TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTCT CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAATGAGTCCCAAATGAGTCCCAAATGAGT CTTCAGCTCTCTTGACATCAAGGCTCTTCGGTCCACATCCACAGACCAATCCAAATTAATCAAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	---			GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGACCTTGGAGACCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/C/TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTGTGTGTTCCAAAGTTCCAAACACAGAAAGTCATTCTCTTTTAA ATGGTCTTAAGTCCAGCAGATGCCACATAAGGGGTTGCCATTGATA
WI-7056b	118	C T	---			GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGACCTTGGAGACCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/C/TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTGTGTGTTCCAAAGTTCCAAACACAGAAAGTCATTCTCTTTTAA ATGGTCTTAAGTCCAGCAGATGCCACATAAGGGGTTGCCATTGATA
WI-7091b	153	A C	---			AATTCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTTATCTGCTCTATAAATAGTATCCAAATCACTGTG CTTAATTTAAATAGCATT/C/TCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C	---			AATTCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTTATCTGCTCTATAAATAGTATCCAAATCACTGTG CTTAATTTAAATAGCATT/C/TCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT

WI-7136	58 T C ---	---	TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCCACTAAGTGTATTGAAGCTGT/CJAATTC TCTCAATAACTCAGTGTAGCACITTAAGTCTGAAGGACAGCAACATGAAGAGGACATATCAATGTG GTGGAGAAAGGAAGGGTGGCTTTTAAATTTATTTCTTCATCTTTTATAACAAGAAAGNNNNIN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTCTATATATG
WI-7146c	210 A G ---	---	GGGACGCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATGOC AACGC/A/GJTTTCATGTACAAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210 A G ---	---	GGGACGCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATGOC AACGC/A/GJTTTCATGTACAAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202 G A ---	---	GGGACGCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATG/A JCAAACGAGTTTCATGTACAAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161 A T ---	---	ATATTACAACCTGCTTTTAGCTGATCTCCATCCTCAATGACTCTTTTCTTTTATATGTTAACATA TATAAATGGCAACTGATAGTCAATTTTGGATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAACNNNNNNNNN/A/TJAAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAATGGTATGTTT
WI-7155	156 T G ---	---	TAGAATAGATGGGTCATATCTCTTGGCTTCTGGCTTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACACAGCTGGCCCTACCCCTATAATGATCCTGTGCTCTAAATTAATATACAC CAGTGGTTCTCTCCCTGT/GJTAAGACTAATGCTCAGATGCTGTTACGGATATTTATATTTCTAG TCTCACTCTCTGTCCCAACCTTCTCTCTCCCACTCCAG
WI-7169b	161 A G ---	---	AGCTCCACCCAGATGCAGATTTGTGTTTGTGTTTCTGTTATCACTGTACACAGCTTAAACATGTAT GCTTTTCAGAAATACAGTTGTCTAGCCCAAGCCATCAAGTGTCTGAAATTCATATTTGTTTATGCAAT ACAGCAAACTTTTATTTAAGTAGAT/A/GJGGAGAAATATGTTTAAATATTTAGGAATCCTAGACCATA TTTCAAGTCATCTTAGCAGCTAGGATCTCAATGGAAGTGTATATATA
WI-7175b	194 C T ---	---	CTCCTAGACTAGTGCCTTACCTTTTATTAATGAAGTGTGACAGGAAGCCCAAGGCGAGTGTCTCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATATGTTTACTGCTGTCTATGCTCATGCTAGCTA/C/JAGAT AATTTATTTGTATTTTGAATAAAAAACATTTGTACATCTCTGATACGGG

WI-7175	194 C T ---	---	CTCTAGACTAGTGCTTTACCTTTAATGAAGTGTGACAGGAAGCCCAAGGCGAGTGTTCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTACTGCTGTCATTGTCCATGCCTA/C/TAAGAT AATTAATTTGTATTTTGAATAAACAATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGCTAGGGGAACAGACAGCAGTGAACCCAGAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATGCACATAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGCTAGGGGAACAGACAGCAGTGAACCCAGAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATGCACATAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCT/AC/TTCTCTCTCTATTT TACTTGAGGCTGCCAATTACAGCCCGCCAGTTTCAGCTCAAGAGATGCCCTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCCTGAAGCCCTAGTACCCCAATT
WI-7182	106 C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCCA/AC/TTCTGAGCCTATCTCTCTCTATTT TACTTGAGGCTGCCAATTACAGCCCGCCAGTTTCAGCTCAAGAGATGCCCTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCCTGAAGCCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	ATAATTGCTTGTTTTCTAGCCTGGCAAGATATTTTATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACACAGCACCATCTAAGCATTAGTGATGGTAGC TGATGTCAAGCTTCATGTGATTTTAAAGCACTCTAGAACAAATGAAGCTTCTTGGCATATTTTAAGGAG CTCCCAAAATGTGTACCTATTAAATTTGTAACCTCAGCAAGTAGAAGACCAATT
WI-7199c	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCCCTCCCTGTGGCCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTGACCTATGAGCT/CT/CGGGCCCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTTGTTTGGTCTGCTGAATTCCTCTTATTAT AGTCTATAGTTTTACTCCTCAGTTCCTCACCATCATCATCTGTCTAA
WI-7199b	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCCCTCCCTGTGGCCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTGACCTATGAGCT/CT/CGGGCCCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTTGTTTGGTCTGCTGAATTCCTCTTATTAT AGTCTATAGTTTTACTCCTCAGTTCCTCACCATCATCATCTGTCTAA

WI-7216c	237	T C ---	---		TGACACTAACACTCTAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTTT/CJCTTGTAATCACIT
WI-7216b	237	T C ---	---		TGACACTAACACTCTAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTTT/CJCTTGTAATCACIT
WI-7220b	147	A T ---	---		AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACACCATATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAAT/TAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTGTT
WI-7220	140	A T ---	---		AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACACCATATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTGTT
WI-7226	232	C ---	---		GATCGAATTTTCAGATGATTCGGAATTTTCATTGAGGTATTTGTAAGTAGACATATATATGTATA TACATATCACCTCCTATTCTTAATTTTGTAAATGTTAACTGGCAGTAAGCTTTTTTGTATCATTT CCCTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAATAATA TTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACITCTTGGGGTTT
WI-7228b	254	G A ---	---		ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAAGTAATGGCTCCAATTCATAA TATGTTCCAGGAGATTACAATTTTGTCTCTTGTCTTTGTAATCTATTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGGATCAGAAAGATATCTTTTGTGCTTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAAATAAGAAATGTTATCCAACCTATTAAAGATATCTCAATGTT
WI-7228a	163	G A ---	---		ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAAGTAATGGCTCCAATTCATAA TATGTTCCAGGAGATTACAATTTTGTCTCTTGTCTTTGTAATCTATTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGGATCAGAAAGATATCTTTTGTGCTTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAAATAAGAAATGTTATCCAACCTATTAAAGATATCTCAA
WI-7233c	213	CT ---	---		CGATCGTACTGCCAGTAGCATTTGTCTGTCTGCGGCTTGTGTTGTACATTCATTTCAATTGTTACA GATGTGAACITTTATCTTGTCACTAATTATATTTAAATTTATTTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTTCTGCCCACCTTTTGTGGCAATATTAAAGTGAACGTGCTAATA GTGTAAGTAC/TTGTGCACAAAACCACTGCCCAGATAACAGAGGGGCTG

WI-7233b	213	C T	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCTGTCGGTCTGTGTGTACATTCATTTCAATTGTTACA GATGTGAACATTATTCTTGTCACATAATTATTTAAATATTCTTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGCCTAATA GTGTAAAGTAC/TGTGCACAAACCACCTGCCAGATAACAGAGGGGCTG
WI-7233	211	T C	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCTGTCGGTCTGTGTGTACATTCATTTCAATTGTTACA GATGTGAACATTATTCTTGTCACATAATTATTTAAATATTCTTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGCCTAATA GTGTAAAGTAC/TGTGCACAAACCACCTGCCAGATAACAGAGGGGCTG
WI-7238	128	T C	---			GGCTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAAGTTTGTTC/TCCGTT CTGTTTTAAACAGAAAAATAAAGGAGTGTAAAGTCTCTTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAGAAACATTTCAGTAGAACATTTTATGCTA
WI-7252f	520	T C	---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGACGCGCGGGGACAGAG GCCTGCCCCGGCGGCGAGCCCGGCCCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252e	552	T C	---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGACGCGCGGGGACAGAG GCCTGCCCCGGCGGCGAGCCCGGCCCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252d	540	T C	---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGACGCGCGGGGACAGAG GCCTGCCCCGGCGGCGAGCCCGGCCCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252c	552	T C	---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGACGCGCGGGGACAGAG GCCTGCCCCGGCGGCGAGCCCGGCCCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252b	540	T C	---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGACGCGCGGGGACAGAG GCCTGCCCCGGCGGCGAGCCCGGCCCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA

WI-7252a	520	T C	---	---	CCACCAGGATCCACAGCCCAAGCGGCCCTCCCGGCCCTTCCACTCGCAGCAGACGCCGGGACAGAG GCTGCCCGGGCGGCCAGCCCGGCCCTGGGCTCGAGGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAAGCAGCCCTAGAGCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCTCTCTGGAGGATGCAGGTGGAACCTCAGTCATTAAGACTCCTCTCTCCA
WI-7265m	252	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCTTT/
WI-7265l	231	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265k	121	T G	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT GTTAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265j	174	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265i	227	T C	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265h	80	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT GTTAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265g	170	T G	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT

WI-7265f	231 T A ---			---	AAC TTGGTATGT CAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTT/AJ/AGGAGTAAGATTGGCT
WI-7265e	227 T C ---			---	AAC TTGGTATGT CAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAGATTGGCT
WI-7265d	174 T A ---			---	AAC TTGGTATGT CAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAGATTGGCT
WI-7265c	170 T G ---			---	AAC TTGGTATGT CAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAGATTGGCT
WI-7265b	121 T G ---			---	AAC TTGGTATGT CAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCCATCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAGATTGGCT
WI-7265a	80 T A ---			---	AAC TTGGTATGT CAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTT/AJ/ATTTGCCACCAAAAGTAATGCAATTTTACCCCATCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAGATTGGCT
WI-7281b	183 C ---			---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGGCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCCTTGGCAAAAACGGAGTCCGAGGCCGCGAG GTGTTGTAAGACCACTCGTCTGTGGTGGGGTCTGCAAGAGGCCCTCTC
WI-7281	171 C A ---			---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGGCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC/AJ/TTGGCAAAAACGGAGTCCGAGGCCGCG CAGGTGTTGTGAAGACCACTCGTCTGTGGTGGGGTCTGCAAGAGGCCCT

WI-7282b	159	G C ---	---	TGTCACCTGGCACATTCATTTTCTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCCTCACTCAAAATATGTCAACTTNNNNNNNT AGGCCCTTTCTAAAAACCAAACT[G/C]TAGCAAGATGCAAAATGCATGGCAAACTCTGCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTCTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTCCACTGAGGTGGAGCATCTCAGTCTCCCCAAATATATCTCCCCACTCCACTAC TCTCTCTCCACTTCATTTTCQ[C]/TTGTCCTTCTCTAATTCAGTGTTTGGAGGCTGACTTG GGGACAACGTATTAATTGATATTAATTGCTGTTTCTCTCCCAATAGAATAAGTCATGGAGCC TGAAGGTGCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGCTGA
WI-7301f	133	A G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTG A/G]CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCA ATCAAATTAIGGACACATGAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/T]TGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTAIGGACACATGAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGT[A/G]TAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTAIGGACACATGAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTAIGGACACATGAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88	G T ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTAIGGACACATGAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG

WI-7301	205 A C ---	---	---	AACATGGCAGTGGTCTGGTTATAGTAGAGAGGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGTTACATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAAACAGCAATCA AATTAACTGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7314c	49 G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAITGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGGTCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAACAAAACCTTGTTTTT
WI-7314b	49 G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAITGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGGTCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAACAAAACCTTGTTTTT
WI-7314	36 A G ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAITGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGGTCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAACAAAACCTTGTTTTT
WI-7321b	199 C T ---	---	---	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /TGTGTTGCTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---	---	---	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /TGTGTTGCTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---	---	---	AGACATTCCTCGTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTTGGGCACATGCTCAGGCTACTATAGGTCCAGAACTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAATTTCTGAATTTTGGGGATTTTCAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAATCA[A/C]CA
WI-7338c	221 A G ---	---	---	CTCTTTCTCAGCACATTCATGGGCAACTAGAAATTACAGCAGTTTCAAACCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTCTTACACAC[A/C]TATACACACAGACATCAGAAATTTCTGTT

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTTGGCAAAAGGTGCTTTTAC/CJCCCTTG AGCCATTATTTGTGCAGAGAACAAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTTTCTCTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGCAGAGAACAAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAGTA GTGTTTCTCTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	221 A G ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAACTCTTAATGATTTTATTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384c	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAACTCTTAATGATTTTATTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAACTCTTAATGATTTTATTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145 T A ---	---	TGAAATCCTGGGCTCTTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTT/AJAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTCTGTCGAAGAACTTTTCCCCCAAGATGTGTATTTGG
WI-7388c	106 A T ---	---	TGAAATCCTGGGCTCTTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTT/AJAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTCTGTCGAAGAACTTTTCCCCCAAGATGTGTATTTGG
WI-7388b	106 A T ---	---	CTTGCTCTGTCGAAGAACTTTTCCCCCAAGATGTGTATTTGG

WI-7499a	33 A G ---	---	CAATTCATAACCACTAGTCTGNTGCCTAA/GJCCATTCCAGACAAACATCCACATTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGCTTCTTTGAATGCTTC ATTATAGCTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAGTAGTCTGGTGTGCTGATTCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAAATAATCATGTGTCATGTATGCAGTAATACTATGTCA GAAGAAAATATTTTAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAGTAGTCTGGTGTGCTGATTCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAAATAATCATGTGTCATGTATGCAGTAATACTATGTCA GAAGAAAATATTTTAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTATGCTTTGGGGTTCTTGATGTTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAATTGCT AAATTGTC/TJGTGAAATAGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATT
WI-7534	135 T C ---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTATGCTTTGGGGTTCTTGATGTTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAATTGCT /CJAAATTTGTCGTGAAATAGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATT
WI-7543b	162 G A ---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTCTTTTGAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCTCTCTTGGCTT/G/AJGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTCTTTTGAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCTCTCTTGGCTT/G/AJGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAAATTTGTAGAGGTC/JCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTCATTTTGAATTCAG

WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAGGCGGTACTAGTTCAGACACATTTGGAAGTTTGTGT TCTGTTTGTAAACCTGGCATCTGACACAAAAA[AT]GTTGAAGCCCTTATTCTACATTTACCTAC TTTGTAAAGTGAGAGACAAAGAAGCAANNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATGACTGTATTTC
WI-7577p	50 GC ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA TAAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATGACTGTATTTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACAC[GA]TAGGAAGAGAGAGATCAAAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATGACTGTATTTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA TAAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCG[GA]TCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATGACTGTATTTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTAC[GA]ACGTAGGAAGAGAGATCAAAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTTAGCACCCACAAATATCAAAACCCACACATAAGTGTTCCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTTAGCACCCACAAATATCAAAACCCACACATAAGTGTTCCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTTAGCACCCACAAATATCAAAACCCACACATAAGTGTTCCTTTCCCTT TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTTAGCACCCACAAATATCAAAACCCACACATAAGTGTTCCTTTCCCTT AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AGAAGTTTCATTTTGGTTTACAC/GJTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTTAGCACCCACAAATATCAAAACCCACACATAAGTGTTCCTTTCCCTT TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTTAGCACCCACAAATATCAAAACCCACACATAAGTGTTCCTTTCCCTTAA AAATATGCATCAAAATCGJ/JTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTTAGCACCCACAAATATCAAAACCCACACATAAGTGTTCCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTTAGCACCCACAAATATCAAAACCCACACATAAGTGTTCCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AGAAGTTTCATTTTGGTTTAC/JACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577b	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTATTACTTTCTCTGAGGGTTTTAGTA/GIACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577	107 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTATTACTTTCTCTGAG/GIAGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7619q	106 C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCTATCCCTCCCTAACGAGACT/C/GTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCT/CJCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90	C G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619j	206	T G	---	---	CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619i	106	C G	---	---	CGCTT[G]TCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619h	150	T C	---	---	CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619g	228	A G	---	---	TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619f	237	G C	---	---	CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619e	99	C T	---	---	CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619d	189	T A	---	---	TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT

WI-7619c	90 C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTCTTACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC[T/G]TCTTTCTTACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCAT[T/A]CTTTTTCCTC TCTCGCTTTCTTTCTTACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATTGGGATCTGTCTTGGC[A/G]TTAAACCATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTC
WI-7626c	155 C T ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATTGGGATCTGTCTTGGCATTAAACCATCATGGACCAAAATGTGCCA TACTAATGATGAGCAATTTAGC[A/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTC
WI-7626b	28 T A ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATTGGGATCTGTCTTGGCATTAAACCATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTC
WI-7626	144 T C ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATTGGGATCTGTCTTGGCATTAAACCATCATGGACCAAAATGTGCCA TACTAATGA[T/C]GAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTC
WI-7689c	134 A G ---	---	---	TCCCATACCGCTGATCTCAGGCTCTGTCTGCCGCCCAACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAA[A /G]TAAGGGGAGATCACACTGGGCGAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAATGGATTTATTAGAAATTCATATGAC

WI-7689b	134	A G ---	---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCGGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTTAGGAGGCCACCCAGCAAAAGGTTGTTCTCTAAJA /GJTAAGGGCAGAGTACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---	---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCGGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTTAGGAGGCCACCCAGCAAAAGGTTGTTCTCTAA AATAAGGGCAGAGTACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---	---	TGGAGAACATTCAATCTTGCCGTCACTATTCAATCAATGAAGATTAGJACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCAACAGCATGGTAGTGCAAAAGAGAGGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCCAGGAAGCAC AGGTCCAAAGGCTGGTCCACACTTATCAGCAGCAACAACTGTCAGTTCATCC
WI-7703b	164	T C ---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAGTAAATTCJGGTCTCTCACTTGTGTTTATTTAACCTCTAAATTC TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T C ---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTCJAAAGTAAATGGTCTCTCACTTGTGTTTATTTAACCTCTAAATTC TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	TTAAATGAGTGTGTTTGTACCGTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCGAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCGCGTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743d	275	C T ---	---	TTAAATGAGTGTGTTTGTACCGTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCGAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCGTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106	C A ---	---	TTAAATGAGTGTGTTTGTACCGTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCGAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCGCGTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275 C T ---			---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGGCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---			---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCTCATCCGAGGAGGGTTCAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743d	275 C T ---			---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---			---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCTCATCCGAGGAGGGTTCAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743b	275 C T ---			---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---			---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCTCATCCGAGGAGGGTTCAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	275 C T ---			---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---			---	TGACATTTATTCAAAAGTTAAAGCAACACTTACAGAAATTAAGAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATCAGTAAAGTTTAAAGTGCATTAATAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAATGAGTAAATTTGTTTATATTTTCCCATTTGGAGTGTAACTGACTGCC

WI-7765b	126	G C ...	---		ACAGGGCCTTTGGCAGGTGCAGCCCCACTGCGCTTTGACCTGCCTCCCTTCATGTCATGGAATTCCTCTCATCTGGAACCATCAGAAACACCCCTCAGACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGGGAAACATTCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTGACTCAAAACCAATCACTGAACCTTTGCTGAGCCCTGTAAATATAAAGGTCCGGA
WI-7773b	237	C G ...	---		TTAATTTACTGATTCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTATCCGTAGTTTGTATAAAAGATTTTCCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGTACTTTGCCATTAAAGGCA GACTAGGGTTTCATGCTCTTTTACCCTTTNNNNNNNNNTGTAAAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C ...	---		TGCAACCTCTTTTGGTATGGGAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAATCAGATCCAGCTTCGGCATTTGATCAGACCAACAGTGTCTTTCCGGGGAGGAAACACTTTTTTAA TTACCCCTTTTGAGGCAACCACTTTAATCTGTTT[C]ATACCTTGTCTTATAATGAGCGACTTAAATGATTGAAAATAATGCTGTCTTTAGTAGCAAGTAAATGTCTTGTCT
WI-7785c	165	G ...	---		GCAGAGACCTTCCAAGGACATATTGCAGGATCTCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAATACTGTAATGCAATGGAAATAAACTGTCTCCCCATTGCTCTATGAAACTGCACTGGTCAATGTGAATANNNNNNNNNGCCAAGGCTAATCCAATTATTATATCACATTTACCA TAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTCTG
WI-7785b	165	G ...	---		GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAATACTGTAATGCAATGGAAATAAACTGTCTCCCCATTGCTCTATGAAACTGCACTGGTCAATGTGAATANNNNNNNNNGCCAAGGCTAATCCAATTATTATATCACATTTACCA TAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTCTG
WI-7785	156	T ...	---		GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAATACTGTAATGCAATGGAAATAAACTGTCTCCCCATTGCTCTATGAAACTGCACTGGTCAATGTGAATANNI- /TJNNNNNNNGCCAAGGCTAATCCAATTATTATATCACATTTACCATAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84	G A ...	---		TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCCACCATCTTACAGAGACTCTCCCTGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCCAAGGACCCATCT
WI-7789b	84	G A ...	---		TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCCACCATCTTACAGAGACTCTCCCTGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCCAAGGACCCATCT

WI-7789	73 GA ---	---	<p> TCTCCCTCATCCAACTCCGAAAGTCTGAACTCTCCAAAGGAGGACCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAATTTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCOCTCTGGTACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT </p>
WI-7790b	190 CT ---	---	<p> AATTGTCAGTCACCTTCTCAAACCTTACAGTCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATCTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTTCTATTTCTTGAAGCTC[G/TT]TCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC </p>
WI-7790	190 CT ---	---	<p> AATTGTCAGTCACCTTCTCAAACCTTACAGTCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATCTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTTCTATTTCTTGAAGCTC[G/TT]TCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC </p>
WI-7795b	81 CA ---	---	<p> CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTGATGATGAT[C/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGACTTTTCTCCAGAAAATTTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCATTAAATACCGTATCTTCTAAATTTGAAATATAATCTG </p>
WI-7795	81 CA ---	---	<p> CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTGATGATGAT[C/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGACTTTTCTCCAGAAAATTTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCATTAAATACCGTATCTTCTAAATTTGAAATATAATCTG </p>
WI-7814c	41 GA ---	---	<p> TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAAAATATGGGATTTTC TTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA </p>
WI-7814b	41 GA ---	---	<p> TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAAAATATGGGATTTTC TTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA </p>
WI-7814	28 GA ---	---	<p> TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAAAATATGGGATTTTC TTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA </p>

WI-7830d	150	C T ---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAAATGTACACATTCATTTTGATAAAATAAATTTGTTGTTCCCTTG AGGTTGATCGTTGTTGTTTGTGTCGCACTTTTACTTTTTGCGGTGGA
WI-7830c	54	G A ---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATAAATTTGTTGTTCCCTTG AGGTTGATCGTTGTTGTTTGTGTCGCACTTTTACTTTTTGCGGTGGA
WI-7830b	134	G A ---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATAAATTTGTTGTTCCCTTG AGGTTGATCGTTGTTGTTTGTGTCGCACTTTTACTTTTTGCGGTGGA
WI-7830	44	A G ---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATAAATTTGTTGTTCCCTTG AGGTTGATCGTTGTTGTTTGTGTCGCACTTTTACTTTTTGCGGTGGA
WI-7865e	25	C T ---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T ---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCCTAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGT ATGCTACTCATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGT[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C T ---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T ---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCCTAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGT ATGCTACTCATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGT[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA

WI-7865	25 C T ...	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGCGAGCAATCTAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191 C T ...	---	---	CCACTTCCTATCTGATTTTCCAGCAAAATGAGGCGAGCAATCTAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92 A C ...	---	---	TTCAACACCTGCTCCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCTCAGTCTCC CTAACAAATTACCTGTCAAGAGG[C/G]AGTGCAGCTCAGGTGGATTAAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCATAAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ...	---	---	TTCAACACCTGCTCCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCTCAGTCTCC CTAACAAATTACCTGTCAAGAGG[C/G]AGTGCAGCTCAGGTGGATTAAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCATAAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ...	---	---	TTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTAAATTTCCCTGCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCACTTCAATGCTAGAT
WI-7868b	173 C T ...	---	---	TTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTAAATTTCCCTGCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCACTTCAATGCTAGAT
WI-7868	66 T C ...	---	---	TTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT [C/T]CACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATTTCCCTGCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCACTTCAATGCTAGAT
WI-7870b	85 T C ...	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTATTAGAAGGG GTGGGGTGGCGGAATCC[T/C]ATTATCAGACTCTGTAAATTGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTGCTGCAAAATGAAATCCAAATGAGCACTAGAAATTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTCGAGTGATTAGAAAGG GTGGGGTGGC/7GGGAATCCTATTATCAGACTCTGTAATGAATATAATGTTTTACTCAGAGGAG CTGCAATTGCCTGCAAAATGAATCCAATGAGCACTAGAAATATTTAAACATCATTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATACAATTG
WI-7889c	54 C ---	---	TTAGGTCTCATGCCACTCCOCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGAAAGTCACTACAGGACTGGCGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7889b	54 C ---	---	TTAGGTCTCATGCCACTCCOCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGAAAGTCACTACAGGACTGGCGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7894c	142 A G ---	---	AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGCTCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTGTGAATTTATTTGCGTATAC ATTATC/AGTATGTAAATTTGCAATTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGCTCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTGTGAATTTATTTGCGTATAC ATTATC/AGTATGTAAATTTGCAATTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTACCTTCAGAGCAGCT GCCACAACTGGCCATG/C/TCCTGCCATTGAACAGTGATTAGTTTGAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTACCTTCAGAGCAGCT GCCACAACTGGCCATG/C/TCCTGCCATTGAACAGTGATTAGTTTGAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTACCTTCAGAGCAGCT GCCACAACTGGCCATG/C/TCCTGCCATTGAACAGTGATTAGTTTGAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC

-157-

WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAGTTTGATCAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAGTTTGATCAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAGTTTGATCAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]JAGACACACACAGGACACATATATAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTGGTTGGCGGTGGTGGTATTGGGCGAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTCTACACAGAGGTAACTAGTCT
WI-7901b	33 C T	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]JAGACACACACAGGACACATATATAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTGGTTGGCGGTGGTGGTATTGGGCGAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTCTACACAGAGGTAACTAGTCT

WI-7901	33 C T ---			AGACTTAGGTACAAATTGCTCCCTTTTATATAIC/TIAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTTGGTGGCGGTGCTGGTATTTGGGCGAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTATACAGACAGGTAACCTAGTCTCT
WI-7901	271 T G ---			AGACTTAGGTACAAATTGCTCCCTTTTATATAACAGACACACAGGACACATATATTAACAGATT GTTTCATCTATTTCCATATAGTATCAAGAGACCATTTTATAAACATGGTAAGACCCCT TTTTAAACAAACTCCAGGCCCTTGGTGGCGGTGCTGGTATTTGGGCGAGCGCGGTGGTGGTGCAC TCAGTCGCTCTGCATGCTCTCTGTATACAGACAGGTAACCTAGTCTCTGT
WI-7926c	150 C A ---			CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAATTCATATTTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCA TACAATGCAATACCTA/C/AJATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T ---			CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAGGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAATTCATATTTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTT ATTTACAATGCAATACCTA/C/AJATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A ---			CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAATTCATATTTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCA TACAATGCAATACCTA/C/AJATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203 G T ---			AAGAGCCAGCAGGTCAAAAGGCCAACACACACCATTAAGCAGCCAGACCCACAAAGGCCAGGTCCTGT GCTATCAGAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCGGACAGATCCCATCCCTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGTCTCAATTCAAATCCATAGATTTTGAAGCCACA GA/G/TJCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCCGAGTGTGCCACCTG
WI-7947	203 G T ---			AAGAGCCAGCAGGTCAAAAGGCCAACACACACCATTAAGCAGCCAGACCCACAAAGGCCAGGTCCTGT GCTATCAGAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCGGACAGATCCCATCCCTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGTCTCAATTCAAATCCATAGATTTTGAAGCCACA GA/G/TJCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCCGAGTGTGCCACCTG
WI-7963b	145 T C ---			CATGTGCTGCATGAAGACTAATTTAAAAAGCAAGTAAGACTAATTTTAAATAAAAATGCC ACAAATTTCAATTTCTCCTTCTAAGTATTACAATGGAGTTTATCTCGCTAAAGTGGAAGAAAT TGAGTGAATGAT/CJAAATTTTGAATTTAGGATAAGATCCAAAGTATTTTCCCAAGTCTTGTTCCTCC CCATAAAGTTAGGCATGAGGAGGAGCAGTCTAATTAAGGCGAGAGACGGAAGAA

[illegible]

WI-8021b	57	C T	---			ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCATCTCGAAAC[CT]GATCCC ACGTCITTAGAACCTTCACCACAAGGAGTTTTCTTGTAGTGATTCCTCAAGAGCTTGGTAGGCATTGGA ACTGGTCCTTTCACITTTAGAGATCTTTCTTTTGGCCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGGGCTTGTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57	C T	---			ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCATCTCGAAAC[CT]GATCCC ACGTCITTAGAACCTTCACCACAAGGAGTTTTCTTGTAGTGATTCCTCAAGAGCTTGGTAGGCATTGGA ACTGGTCCTTTCACITTTAGAGATCTTTCTTTTGGCCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGGGCTTGTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A G	---			CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCATCAACAACAACCATTTTCAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTAGAACAGCTGGCCCTGGTCGTGCTCAGTACACAAGGAAGAGC
WI-8024b	206	A G	---			CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCATCAACAACAACCATTTTCAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTAGAACAGCTGGCCCTGGTCGTGCTCAGTACACAAGGAAGAGC
WI-8077	167	A G	---			GAATGAGCCTTCTAGCGCGAGGAGCTGCTGCTGTTGTGGCTGCACATGCATTCATGGAATGC TTTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCCAACTCCTTTCT AAGGAGCTGGGTGTATGCTGCTACAAACCA[A/G]TAATTCATCAGATGGATTTTATTAAACGTT GTGATTTGACTTACTTTTCCAACTGACTCTGGCATACAAAGGAAAAA
WI-8118f	114	G C	---			TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTGTTT[G/C]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	---			TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGC TATGTAATTCATGCTGTGGAACTGGCAATACAGAATGAGCTGTTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	---			TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTGTTTGTGTTT[G/C]TTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAATCAAAGCAATTGTCANTTTGGATTTTGGAAATGA[C/T]CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAAATACAGAAATGAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCGTATTCCTGCTCCTCCTATTCCTTCCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAATCAAAGCAATTGTCANTTTGGATTTTGGAAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAT[C/G]GCAATACAGAAATGAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCGTATTCCTGCTCCTCCTATTCCTTCCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGAGGGCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGAGGGCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTGGGCTGT TTCTCTATCTAAGGG[C/G]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAATTC TGTGATGATGAAAGATTCTACTTCTGACCTATTCATAGGGTAACCACT
WI-8314	78 C G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTGGGCTGT TTCTCTATCT[C/G]TAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAATTC TGTGATGATGAAAGATTCTACTTCTGACCTATTCATAGGGTAACCACT

WI-8321	178	G A	---			TTTTAAATATGCCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATATAGTACTGTGAGAAG TCCCCCTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAITG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A	---			TTTTAAATATGCCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATATAGTACTGTGAGAAG TCCCCCTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAITG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C	---			TATGTAACCTACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTGTCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCCAAGTCTTCCCTTCCCTGTGC/AJGCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTTGTTCCTCCAGCAATGCCTACTGAGTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C	---			TATGTAACCTACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTGTCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCCAAGTCTTCCCTTCCCTGTGC/AJGCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTTGTTCCTCCAGCAATGCCTACTGAGTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C	---			TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATAGA AACTGCCCCCATGATCCAAATCACTNTCACCAGGCCCTCCTCCAAACACGTTGGG
WI-8378	308	T C	---			TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATAGA AACTGCCCCCATGATCCAAATCACTNTCACCAGGCCCTCCTCCAAACACGTTGGG
WI-8426	184	T G	---			TTTAGCACATATTTAGCATTAAGCCTCAAAGATACAGCAATATGTTACATCTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTGACCNITAA GAGGNTCTTTTGTGTGGGAGGGTGGCTTTGCTTGAACCTCATCTGT/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCGGGGGCTTGGCNATGNATCAGTGAG
WI-8450h	61	C A	---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTCTACATACACTC/AJCA TCTTCTATCTTAGTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTTAAAGA AAAAACCTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55 T C ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTC/AJCA TCTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A/G ---	---	CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAGAGTTACAAAAATACGTTATTTTAA/JGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGATACATTCGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATCTTGAAAACTTTATTGTCACAGT GACATCCATTCGCCAGACTTAATGTTATAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---				CTTCCTCCTCCAAAATCTACATGAATACCTGAAGACAAATATACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTT[AT]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461b	38 T C ---				CTTCCTCCTCCAAAATCTACATGAATACCTGAAGACAA[AT]CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCATTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461	38 T C ---				CTTCCTCCTCCAAAATCTACATGAATACCTGAAGACAA[AT]CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCATTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461	105 A T ---				CTTCCTCCTCCAAAATCTACATGAATACCTGAAGACAAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTT[AT]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTCGAAAAAGGGGG
WI-9438	77 A G ---				AATAACATGTTATGAACAAGCTGGTTACAAGTAGGTAGATGACTTAATTTTGATAAAAAAT TAAAAAGCAT[AT]G/AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATCTTCCCTTGTGTTTGTCTTTTAAAAACATTATTTCTGAAAAAAA ATCAGAAAAACATGATCGTGGAGAAATTATTA
WI-9439b	101 C T ---				ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAATCCCAGTCTGCAGCTCAGTACCTGT[AT]GTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTAGAAAACAGCCCTACCCCGAGAGGGTCTCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAAAACAAAG
WI-9439a	76 C T ---				ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAAT[AT]TCCAGTCTGCAGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTAGAAAACAGCCCTACCCCGAGAGGGTCTCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAAAACAAAG
WI-9446b	75 T C ---				GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAA[AT]C/CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAGCAAAACCTTTTAAAT TACTCATCTTCATATGTGTGTTGTGNCCTACTNTATCACTGTGCTCTGCTGCTTTGCTACCTA TGNGAACTGCACACTA[AT]CTGTGGCAATATGT

WI-9446	75	T C	---	---	GAAGGCTTGATTAAAGGGAGGNTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAATTC/CCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTTTATATGTGTGTTTGNCCCTACTNTTATCAGCTGTCTCTGCTCTTGTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A	---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTTAGATTCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTACATGGAAAAGCCCAACAAATAACTAAACCTTGACTAATGSAAG
WI-9497	185	A	---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTTAGATTCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTACATGGAAAAGCCCAACAAATAACTAAACCTTGACTAATGSAAG
WI-9523b	193	C A	---	---	GTGAAAAAGTTTCTATTCCATCCATCATAACAATAGATTGTGCTAAGGATCATTTTGGAGAATGTG CAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAATTACAAACTATTTAGCCCATGATCTATGGTGATTTTCCACACATTTGTA/C/AJAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A	---	---	GTGAAAAAGTTTCTATTCCATCCATCATAACAATAGATTGTGCTAAG/G/AJATCATTTTGGAGAAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTTAGCCCATGATCTATGGTGATTTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C	---	---	AAAAACACAAGTTTTCATACATCACAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCTTNNCTAGTTGTTATGTACAAATGCTGTAGATAATGCAGCCCCATG CAATACACCCCAAGAACACACTAGAGTCTACCCCAAGTACATATGATAAAGCAGCCCTCTGCAAGTG GTT/C/GCTGGTATACCCTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G A	---	---	CCAAAAGCCCAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTGTAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/G/AJTTGAAAAATCAATTTCAAGGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCCAG GGNTAAAATGGTACAAAAAAGGCTGTAACTCTTTNCTTCACATTGATCACA
WI-9625b	172	A T	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAACCTTTGGAAAAAATAAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTIA/TGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTC

WI-9625	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTTGGGAAAAAATTTGGAAAAAATCAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTATGTTTACCAATTTTATATGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACAACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTTGTAAACAGTGTATTGCTAGACCTAAATAATCCAAGCT TACAACCT[C/T]GTCCCTTACCTGTATACATTTATTCATTTACTTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCCTTTTCAGATGTCCTGCTTTTGTAAATGTTGTTT
WI-9676n	114 A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCA[AG]GATGTGGCTTTCCCTGCC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676m	184 G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGC[G/T]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676l	84 A C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676k	202 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676j	92 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676i	173 T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTT/C]CCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT

WI-9676h	134	C A ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ C/AJATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTTCTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ C/AJATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACACTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGATAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGACCTTGCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACATGTCGTATGCTGTC
WI-9738	40	C A ---	---	TGGACCAACACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACACTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGATAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGACCTTGCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACATGTCGTATGCTGTC
WI-9756	47	A ---	---	ACTGAAATGTAATGGCCAAAGGCCACCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACATCAAAAGCATCTAACAAGAGCAGGATGTGATGTAATGTGCCCTTATCATTAGTC AGTAAGATAAGAAAGCCCTGGTGAATCCACTCCACAACACACAGATAATACACTTTTGGGAA ATTCCACTTAACCACTTGATCTCTCACTTTTTTATGATTTAAACTCTCCGTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTGCAATGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAAAGAGAAATCTTGTTGCAAGGTCAATTTTATACTATTA A[A/G]TAAAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTAAATCCAGGCGGGGAAAAATGGATACCTTCATATGCTCTGACCCAACTATAAATTTTG GTTCTCATGCACCAATTTTCAATTTTGCCTTCTCACTCCAAAGTACCAGTATTTACCAATTTG[A/CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCTCA AAGAAATGTCAGTCAGGACTAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCTCCCTTTTGGCTCTCATGCGCACTCCCTCAGCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAAATGCAGTTT[C/A]TGGATCCCACCCAGGA CTCAAAAAAAGTAAAGTGGGAGAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAGTGGACTAAAGTTTGAGGACCAAGATGGAAGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC[A/G]TGTGTATGATATATATACTATTAAACACTT AGGATTATATACACACAATAAAACGCTCTGTAGGATAAACTAAGGTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTACTTGATGCTGTTG
WI-9880c	222	G A ---	---	GAACATAACACTTCTTGCAATGGATTTTCTTGATATTGGCAGTTAACAATAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A	---			GAAC TAACACCTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACATAAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTATGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC/AJATATATAAGATCCTCTTTTAAATATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T	---			GAAC TAACACCTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACATAAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAATATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
						ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACCTTGGAAATCACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAACAAACACGCCCCAGTTATCACAGTTCTNTTTTGTCT/CACCC ATTTCCATAACAAAAGAGCTACACAAAATNGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTGATGAATAATGATTCCAAA
WI-10183	127	C T	---			TCCTCAATGACAGATGAACATAATTTCTCTGGGTAGAAATACCTTTATGTCCATTTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAGAAATGGAA/JGTTGATTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTGGATATCC GGAC
FB25G10b	109	A G	---			TCCTCAATGACAGATGAACATAATTTCTCTGGGTAGAAATACCTTTATGTCCATTTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAGAAATGGAA/JGTTGATTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTGGATATCC GGAC
FB25G10	109	A G	---			ACAACGCTGAACCTTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAAC TGAAATTAAGNTAAATAAAATAAAATC/AJCAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTCACCTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCTATTAAACCCAGTCTAGGGATTCTG
IB3071	102	C A	---			CGTCTTTCTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAAATGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTACTTAGGAACCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGTCT/JTGACCACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTC
NIB551	161	C T	---			AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGGAAAGTTCCCTTTG/JAATTTGTCAGTTC ATTCCTGGAATAATCTTTTGAGTTAAATAAGGATCCTAGGACAGACACCTCGAACTACAGGCCCTAAA GAGAAATTGCTCAAAACCAAGCTGTAACCTCTCCCTTTCTGCAATTGGTTGCTTTTAAATA TTGCAAAAGTCTGTGATGCTAAACAGTATTGGAGTGTTCAGTGTCTGTA
S72904	51	G T	---			

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAACCCATTAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGACCTTACACCTTTTGATATGTAAGCTTGACCTAAAGTCAAGGGACCTGTGTAGCATTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTGTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTTCCTTTAATTGTAAAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCCTCTTT
ESTC122	34	---	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTGAGAAAAACACACTGAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCGAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTGGTTAIGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAACNCATGTGTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	---	CCAGTTGGCTTCTGTCCTCANAGTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	---	AGGACACAGCCTAAGGACATGAAGTCAGAGTTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	---	CCCATTGTGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTTCATTTTAAATC AAAGANACCATTCCATTTCCTAACAAACA
ESTC143	29	---	---	---	---	GTTTACGAAAAGTACTGAAATGCTATTANTAGCTGAATTTTGATTTTCTTTTG
ESTC144	26	---	---	---	---	AAATCCATATTTTCTTGACATGAGGNGCTTTTAGCAGCATTTCCG
ESTC146	20	---	---	---	---	CATGTCAGGATAAGGAGCANACACAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	---	TCTTGGTTGTCTACACAGACACTTAAGTACTGTATGCTGTATGACGGCCTGTGGAGGCCCTGTG GGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	---	TCAGTTCAATTTATTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	---	CCAGGAAAACAAGCAGACACANACTTATAGAATCTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	---	GAAGCTAAGGCCCATTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	---	TTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCAATTTACA
ESTC156	32	---	---	---	---	GCAGCAATTTGTACAGGAGAGCGCAAAACAAANCTGGCTGCCGATGGAGCGGGGGGGCCTCA CCACCACCTGCAT
ESTC158	35	---	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	---	AGCTGGCAAGAGACTTCTCGAGGACATCAGTACGTTGGTCAATTTAGGCACGCTGCTGTTCTGCA GCITTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCCACAAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATGCTGGTGAGTGGGGGCTGAGCTGGGNGCAGTGGCAGTGTCACTGGGCCGTTTG GGACTGGGTGA
ESTC162	36	---	---	---	---	CTCTTCGTCGGTTGCAAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAAATATGGTTTTGTAAACNGAATACAATCCAATATATAACATTAACAAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCCTGGTGTGACGGGAATCANITTTGCTGGATTAGAGGAAGGTGCCGCTGTGTTCCATGACTT
ESTC176	23	---	---	---	---	CACTCTCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCITTTATTTCTATTAATAACCTTTTAT TCTCTTTATCCCATAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGGCGACATCAGCATTGTCTCNITGTACAGTCCCTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAAITGTCAATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCTCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	---	TCTATTAAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATCACTACTGCTCTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACTTTCCCTTAACCTATATCAGTCTAGTAAGCNTTTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCTCTCCCTCCNGCAAAGTCTCCCAACAGCACA
ESTC20	33	---	---	---	---	AAGATTAGACAGACCGGTATAGTAAGCTCTGNGGAACTCCAAGATCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCTTTTGGCTGCAACAG

ESTC201	35	---	---	---	---	TCTTACTTGGGTAGTTTAGCAAAACATTTTTAAANCCACATCCACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGGACAGACGCGNCGGCGCTGGGTGGCGCCCCAGAAAGCGTGGCGTGATGTT
ESTC203	27	---	---	---	---	CGAGATGAGOC
ESTC208	43	---	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC
ESTC210	29	---	---	---	---	AAGACACGTTGCA
ESTC212	27	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGGATAANAGCAATAACTATTGTTTAAAGC
ESTC214	21	---	---	---	---	CTAAGAGTGAATA
ESTC216	49	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAGAAGTGAGTGACGGTGACCTGTG
ESTC217	28	---	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT
ESTC219	32	---	---	---	---	TCAAGTC
ESTC22	41	---	---	---	---	CTCCAGAGTCCCTCCTCTCANACCAGGGGCAGGAGGAGTTAGGGAAT
ESTC223	27	---	---	---	---	TGGCAAGAAATTTATTTACACTAACAAATTAATTTAATCACAGGTTATTAGATTGGTCAGAAAA
ESTC224	37	---	---	---	---	CAAAAGACCA
ESTC225	20	---	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAAATAACATTAACAAGTTCAT
ESTC23	27	---	---	---	---	AAACACACCCCA
ESTC230	43	---	---	---	---	GTACACATCCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG
ESTC231	24	---	---	---	---	GCAAGGAAGC
						TCATTGAAGAAAAATTATGGGTTTTATTCTTATTCTAATTNGAGAAATGCTTAATGTCACAGGCTACA
						TAAGGGCC
						CTTCTGAAGCCCAAGAGAGGGGCAGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGAGGAGGA
						CGAAGGTAGATTTCCTCACATATTACAAAAATACACANAAACACACACACACACACACA
						TGCACGTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGTTCAGAAGGA
						ATGTGTAGGATCG
						TTCCTTTTATTTCATATCCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT
						TCCTGAAGGG
						GCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGAGGCCAGAAATTAAGA
						CAAAAGGGTTAGTCATATCCCCCANCAACAGCATGATAAAATAATTC AAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTCTCTATTCCTATAAAAAATAAAGGAGCAGAAATCTGC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTATCTTGAGCCGCTTGTCAGGTTTGATTCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATATNTCAGTCGGTGATCATTGTAATATACAATACAAAGCAATTTCTCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTGACGTTGTNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTATGCTGATGGAAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTGTCCCTTCAC
ESTC45	37	---	---	---	TTTGAGGTTTGTGCTGGAGTTTGTCTTTGTAACNCTCATCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGTGAGCCCTGCCGCTGTCCATGGGCCAGGAGCCACTGGTGGGANCCGGGCGAGATGTTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCAAGT
ESTC57	20	---	---	---	AAGTGGCCCTCCAGTCCNCTCTCTGGGCACAGATCCCACCACTGCTCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTTCCAGACTTCAGGAAAAATGATTTCCACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTGGCTAGGCGTGTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCCACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCNAGGGCCACGGGAGGGTGGGGAGACGACACTTTTCCCTGGGAAAAGGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGTCACITTCGGTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCTGAGTTGCANGCAGATGGAGATTTGGACACTG

EST10398	147 C T ---				TGCTGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGGGGCCATGGTA
2a	14 G C ---	---			AGATGCTGCCACCTCTTATCTACTTATGATGATGTTCACTTTGGGGCTTGACATTTCCAACACGGAGAAG
ESTD-C7					CATTGTTTCTTTC/TGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCAATTTG
ESTD-					ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGGA
D4S95	90 T C ---	---			CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAATTTTGAGAAGAGCAAAACAACCTTTCAAGG
ESTD-					ATAATGGGGCAATCACTTCTTTT/C]CTTCTTTAGAGTCTACCGG
GPPK2L	38 G A ---	---			AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTTACC[G/A]CCGAGAACTGCTCGATATC
ESTD-					CTGGGCTGCGCGCAGCAGCTGCTGGCACTGGACGGCGGCGCAGGCTCAOCTCTATAGTGGGTCG
HRASb	82 A G ---	---			TATTCGTCCACAAA[A/G]TGCACTCTGGATCAGCT
ESTD-					CTGGGCTGCGCGCAGCAGCTGCTGGCACCTGGACGG[C/T]GGCGCCAGGCTCAOCTCTATAGTGGGG
HRASa	37 C T ---	---			TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-					GGAGGCAGGAGGTGGGGAGGGGCTGCTGCTGCCAGGTCCACACAGCAGAGAGGCGCCTCAGTG
NRAMP	81 A G ---	---			TATCCCAACCCCA[A/G]TGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G ---	---			GTGACCTTCTCACTTTAA[A/G]AAACTTTACCGGAGAAGAAATTAATATATGCTATGGCTATCAGC
EST36751					AGATCTGAATTTAGGATAAAACAGAAAGGAGAGGTATGTAAACA
7	36 C T ---	---			CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT[C/T]GATTACTTTTCTATTCAAATCTCTGTA
					AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
					CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAAATCTGCCCAAACCTTGTGGCTGAC
					TTTATGGCTAAGAAGTTTCACTGGATGCATTAAATAACAAT[A/G]TTTACCTTTTGAAAAATAA
					ATGAAGGATTTGACCTGCTTCGCTCTGGAAAGAGTATCCGTACCGTCTGACGTTTTTGAACAATACA
EST40562	109 A G ---	---			GATGCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
					GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA
EST18288					GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA[C/T]GGGAGCCAGT
3	121 C T ---	---			GTGGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAAAACCTCTCTGCTGGCTC
					TGGCCCTAGGACTTAGTATCC
ESTD-AK-168	31 C T ---	---			GGGAGTGACAGCTAGAGCAACCAAGGGGGGCT[C/T]TACAGCTGTGTCTCATGGAGGACAGGCTTCT
					GCTCATTTCTGG
					AATCCCAGCACTTTAGGAGGCTGAGGCAAGGCATATCACCAAGGTCAGGAGTTGAGACCAGTCTGA
					CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGTCATGGTGGTGCATGCCTGT
ESTD-ALB	180 A G ---	---			AATCCCAGGAGGCTGAGGAGGAGGAGTTCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAGCCGA
					GATGGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGCTTC

EST70523 3	182 G T ---			TTCCGGCAGCCCCCATCTTGGCACCCCTGGTCCCTCAGGGGCAACCCGGGCACCTACCGCTCTCGCTCGGTAAACATCCGGCCGGCGGCGCTCTTGAACATAGCTGGACGTTCCGTATAGGAGGACCGTGTAGGCTTCTGTCCGGGCTTCCAGGGGCCAGCCCTG/TJGAGAGAGAGGGGTCCCTGTGGTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
ESTD- APOA2	101 C T ---			CCAGGTGTTGTGGCACGTGCCTGTAATCCAGCTACTCTGGGAGACTGAGGCATGAGAATCTTTTGAACCGGGAGGGGGAGGTTGCAGTGAGCTGACATCG/TJGCCACTGCACCTCCAGCCTAGGTGACAGAGCAAGACTCC
EST58707 7	112 C T ---			CAGTGTATCTGGAAGCCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTTAAGTTACGATCTTTGGCTCACATGAAGGCCAAATCCGAGAGAC/TJCTAGAAAGATACACAGAGACCGAATGTATCAAAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCACACTTGTCACTACATTTCTGATTGGTGGACTCTTGTCTGCTAAGAACCTT
EST74167 6	137 C ---			AGACCATGAAGGAGTTGAAGCCCTACAAATCGAACTGGAGAAACAACCTGACCCGGTGGGGAGGAGACGGCGGACGGCTGTCCAAGGAGCTGCAGCGGCGAGGCCCGGCTGGCGCGGACATGGAGGACGTCCGGCGGCGCTGGTGAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCCGAGAGCGTGCGGGTGGGCTCGCTCCACCTGGCAAGCTGCGTAAGGGCTCCTC
EST43211 8	132 C ---			CGCCTGTTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGGGTGGCCTCGCTCCACCTCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCGGATGACCTGCAGAAAGCGCCGTGCAGTGTACAGGCGGGGCGGCGAGGGCGCCAGCGGCTCAGCGCCATCCGCGAGCGGCTGGGCCCTGTGGTGAACAGGGCGGCTGGCGGCGCCACTGTGGGCTC
ESTD- APSB	126 A ---			GGAAATAATGGAGCCTGTGGGAAGGAGGCGTCCGAGGGTGGGCTTGTGGCAAGCCCTTGCTGAGACAGAGGGCGTGAAGACCCGGAGCTCATCACATCTCTGACTGGCTGCCAACACTCATGAAGCTGGCCAGGGGACACACCAATGGCACAAAGCCCTCGGATGGCTCGACGTGTGGAAACCATCATAGTGAAGAACCCATCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144 C ---			TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCCATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAATTCAACCTCCCGATAGGGCTGGGCTGACCAAAATATACTGGGTTTCCGTTCCTTTTCTGATCATCTTACAAGTTATACCTTATTGGAGGCCCTAAAGAAAGGCTTATG
EST26021 1	137 A ---			TAATGTAAGCTCATCCCAAGAAGCCTGCACCATGTTTGGGTTGAGTGAGTGTTCGAAACCTGTCCATAAAGTAATTTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCTGAACAAAAGCTTTCTTCTTTTGCACAAAGACAAAGCAAGGCC
ESTD- BA511	29 A G ---			GGGCAACATAGTGAAACCCCATCTCTACA/AVGJAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGCCCTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAGTGAGCCAAGATGGTGCCACTGCA

ESTD- CB22	119 C T	GGCAAGTTTTATTGATAGAGAGGAATCAATTAATGGCAATGAGGAGACATCACCTGGAAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGCTGGATGGATACAAAAG ACAGGCAAGGAAGGTAGAACCATCAAGAGAAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTTATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACACAGAGCT CTCAGAGAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAAAAACGTTCCCAACCCGA GGTGGCTGTTTGGCCATCAGAAGCAGAGATCTCCACACCCAAA
ESTD- CB24	145 A	ACCAGGACAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAA AAAGTGTCCACCCAGGTGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACTGGTATGCTGGCCACAGGCTTACCCGACACGCTGAGCTGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G	GTITCTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTATCTTTCGCCGTG TCTGCTCTCGAACCCAGGATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTAGTCTACATGCTGTCTTGTCAACAGAGCTTACCAGCAAGGGTCTCTGTCTGCC ACCATCTCTATGAGATCTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD- CB27	125 C T	TTTTCTGTTCCCTGAAGATTGAGTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTGCATTTCAGGAGTGTCTGGAGTCTGCTCATCTACCTGACCTGATCTTC TGATTAGGGAAGCAGCATTCCTTGGACATCTGAAGTACAGCCCTCTTCTCTCCACCCAATGCT GCTTCTCCTGTTCTCTGATGGAAGTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATATGTA TTTCTTAAACAATAAACTTGAAAGTCCAAAATTAGTCTTGATCCATGGACTGCAGAAATAAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATTTTGGAGGAATCTTGTTCATGCAATG
ESTD- CYP2D6	61 A G	CAGGCCAGCGTGGTGGAGGTGCTACCATCCCGGAGAGAACAGGTACGCCACCACTATGCAAGJCA GGTCTCATATTGAAGTGTCTCAGGGTCCCTTGGCTGAGCAGGGCCGAGAGCACTACTCGG
ESTD- D11S1873	40 A C	AAAAAACATTTAACACCTTTCAATCATATACACCATA/CJATTTCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTAATGCAATCTAAAATGTCATAACTGATTAAATGCAAGTTCAACAG ACAACCTTCCCAAGCATCTACGATCAGAAAGTCAAAATATTACATATCTGGATTAAATATGCCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T	CATCCCCAAGCCCATCTTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGGGTG GGGTTGTGGCTATGGTGGTCTGTGTAGAC/CTGGGGGCTTGGTTTCAGTTGCACTATTGCCGT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCCTC

ESTD- D17S33a	75 C T ---	---	CATCCCCAGCCCATCTCTTAGCCACTGGCATTCTTTGCGGCTCTGACAGATACACTCAGGGCGGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGCG GTGGGTTGTGTGGCTATGTGGTGTCTTGTTAGACGGGGCTTTGGTTTCAGTTGCACATATTGCGTT ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCTGGCCCAACATGGCGAAATCACATCTCTACAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGATTGCTTGAACCC[A /GJGGAGGCAGAGCTTGACGTGAGCCCAAGATCACACCACCTGCACCTACAGCCTGGGTGACACAGTGA GACTCTGCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAAAAATCCAAATAAGTACACTGTATAAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCAGTTATTTATTGGTAAGCCATACATAATTCTAAAGCATGTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATATTGCTGATGTTGCTGATGTTCCJAGJGGAGCCTTGATGTGATCTCTGATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAACTCTCTACAGCCGTTGTTGTTATTAAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACATGACCCAGACCTGCTAGCAGAACATTTCTGCTG TGAGTCTTATTCAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAACATACCTGCTCTAGAACCCAGAGTACATGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGCTCTTTATTGGAAGGATGCCTJGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACATGACCCAGACCTGCTAGCAGAACATTTCTGCTG TGAGTCTTATTCAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAACATACCTGCTCTAGAACCCAGAGTACATGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGCTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGJGTCTCTACATCATCTTTCACAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGCTGTCGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCTGGGAGAGGAGGAGGGAGTGGGAGGGAGACA GAATGCTGATTJACJCTGTGGTGAGAACCAAGTCTGTCCTGTGGGTAGGGGAGCTGCTTCCAAAG ACCTCCTGATTGAGGAAGGGGAGCAGCAGAGCGCAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGCTGTCGCTCAAGCAGCTGCTCGGCTCCACJ GJTTCCATGGGTGTGGGCTGGGACCTCACTGTCCTGGGAGAGGAGGAGGGAGTGGGAGGGGAGA CAGAACTGCTGATTATCTGGTGAGAACCAAGTCTGTCCTGTGGGTAGGGGAGCTGCTTCCAAAG CCTCCTGATTGAGGAAGGGGAGCAGCAGAGCGCAAGAGAACAGAGT

ESTD- DRD1	154 C T ---	---	TCCCCAGCCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAGATCCAAACCCATCAC ACAAAACGGTCAGACACCCAACTGAACTCGCAGATGAATCTCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGC/TTCGCTATTAGAACTAAGGTAC
ESTD- DRD2	144 C ---	---	TCTGCCCTTGGTGCAGGAGCTGCCGGGAGGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCACCCACCCAGCTGACTCTCCCCGACCCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCGCCCAACACAGAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	AAGACGATGGCCAGGATAGCGCGCAGTAGGAGAGGGCATAGTAGGCGCTGGGGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTACAGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCACAGAGGGAGGTGCGTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---	---	TCTTCAGGATCCGATCTGCCCTGGTTGGGCATCGCTCCGCTAGGTGTACGCGCTCCACAGCTGG GGTAGGGGGTGGTGGTCAGTG/C/TGGGGGCGGTGCAGACCCACCGCGGCTGGGAGGACTTCA CCCCGCTCACTCCGTTTCTCGCAGCAGTCTCCGCTCGTACT
ESTD- ETS2	43 A G ---	---	ACTCACAGTGCCTTTAAGTGAAATGGTCGAGAAAGAGGACCC/A/GJGGAAGCCGCTCTCGCGCTG GCAGTCCGTGGGACGGGATGGTCTGGCTGTTGAGATTCTCAAAGAGCGAGCATGCTGGACACA CACAGACTATTTTAGATTTCTTTTGCCCTTTGCAACCCAGCAAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAAACAAACCATGTCTTTTTCAGAGTTAGTTG
ESTD-F9	111 A G ---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGTATGATGTTTA/A/GJGTCAAACCTTCATTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACCAAAAAAC
EST68787 5	144 A ---	---	CTTCTATGGGATTTGACTTTATTTTCTCCATTTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAATAAATTCACAGTCAA AGAATCAAGCACTTTTGAACATTTGAAGTTGTTTTTGAAGTTGGTGTCACTTTAATACAACTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GCDH	200 C G ---	---	CGCAGACCCGGTCAGTGTGGGGTCGGGAGTGTGGAGGGAAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGACAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGGCACCCTGTGTTCTGCTGCCCTGTTCAGCTGTCTGTCTGCCGAGT/C/ GJGACTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	88 A G ---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGTTGAGCCCTGCTGAGGCCACTCTCTGGTCACCATGAC AACACAGGCCCTCTCAGGA/A/GJACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAAATGCCAGCGGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTCCCCCAGGTACAG

EST34088	62 A T ---	GTGGGGCAACAGTGGGAGAGAAAGGGCCAGGGTATAAAGGGGCCACAAAGAGACCGGCTCJAVT
ESTD- GNAT2	56 A G ---	AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD-HT2	154 G ---	GACCCGTAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGTCAGGGTCAAAACCCACJAGJGGCATCA TTGAAACCAAGTTTTCCGTCAAGGACITTGAAITTCAGGTAAGTGCATGGTCCCTAGG
ESTD-HT5	149 C ---	GGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTGACTTGCACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGTACAGAGAGAAATAAAGGATAACCTGGGTTTTCTGTGC TTTGCTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACACGA AAGCGCAGTCGTGAAGTTTTCAACAAGACACACCTT
EST37382	124 A G ---	AACACAAAGCCCCAGCGAGAAITGAACTCGGACCCCTGGTTTACAAGACCAGTGCTTAACCCCT GAGCTATGGAGCCCCTCGTCTGCTGTTGGTTTTCTCTTCACTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCCTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGTTCT
ESTD- IGFBP1	43 C T ---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCACCCCTCTTTCTCTCTCCCTGGGA CTTTGAGTCAAAATTTGGCCTGGACTTGAGTCCCTGAACCAGCAAGAGAGAAAGAGJAGJCCCCAGA AATCACAGGTGGGCACGTGCGCTACCGCCATCTCCCTTCTCACGGGAAITTTACGGGTAACT ACCCAGTGGAGCCCGCTCATTCGACGGTCTTGGCAGGAGGTGCJCTCTGGGAGAGAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	TTTACTATTTCAATGATACAGAAATTGGGAGTCACATAATTCTATGAACAAAAATTCAGATTT CAGTGTAAATGTTGCCTACATTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGTGGTGGG TGACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTAATTATTATTATTTATTTTGTG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGCAGTGGCJAGJCAATCTGGCTCACTGCAAGCT CTGCCTCTGGGTTTCATGCCATTCTCTGCTCAGCCCTCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	99 A G ---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTACCTTGGGTGCTGTTCTCTGCCCTCJAGJGGAGCTCTCTGCAATTGCAGG
EST374082	124 A T ---	TCCAGGGTGGCTGGACCCCAAGCCCAAGCTCTGCAGCAGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGGTAGCCCAAGGGGCCCCAAGGCAGGCGACCTGGCTTCAGCCTGCTCAGCCCTGCTGTCTJAV TJCCAGATCACTGTCTCTGCCATGGCCCTGTGGATGCGCCTCTGCCCCCTGCTGGCGCTGCTGGOC CTCTGGGACCTGACCCAGCCGACCGCTTTGTGAACCAACACCTGTGGC

EST45311	151	C T	---			GCCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCTCTATTAAGTGAACATACATGCAATCTCTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGGAAGGATCCACGTGTGGCCCATATTGTAACA CAATTTCTGCAATC/TACCTCTTTCATTTAACAGCCCTTATCAATGGCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258	80	A G	---			TGCCCCATCAGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCAG/CCTCAAAATGACAGCCATGGCGCGCGGTCTCTGGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCAGCTTTGCATGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGCTGATTAA
EST38216	26	A T	---			ATGCAGGATGAAGGTGGACAGGGAGG/TGAGGGCCCAACCTGTCTCCAGGGCTGCAGATGTCG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149	G T	---			ATACTAGTACAAAGTGGTAATTTGTACATTACACTAAATTAATAGCATTTGTTTAGCATTAACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTG/TAGTGCCAGTATCCAGAGTTTGGTTTTGAACCTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTGGTGCATGCA
ESTD- KRT10b	183	C T	---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTGAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG/C/TGTGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133	A G	---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTGAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTA/A G/GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTCTTTTAAATAGTC TCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231	C T	---			ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGGCCAGAAATGTTAAGTACAAAGTGAGGCCCATAG GCTGCCCTATCTCTCCCGTCTCAGGTTTACCA/C/TGTCAACATTGACACA
ESTD- KRT8a	21	C T	---			ACCTCACCCCTCCCTTAGCC/C/TGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGGCCAGAAATGTTAAGTACAAAGTGAGGCCCAT GGCTGCCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099	82	C T	---			CACTTGTGTGTAGATCTCTCAGTGGCGCTCTACTGGTTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TGGGGCAACCCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCTTGGCGCTCTTGGAGGTGTGG

ESTD-LF79	142 A G ...	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTAAACCGTAGCAAAACGTCATTGGTATTAGA AAATAAAAATTTCCAATATGTAGTCTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCA/GGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ...	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG/A/CACAGATTCTCTGGAAGACAGCAGCGGGATGGGGGAGGAGAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G ...	---	TACACACTTTCCTTACCCATTCACTGAAACGACTC/G/GCAAACCTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113 C T ...	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTCTTCAGCTCTGCCCTGCTGCTGCCTGCA AGGGTTTGGCTTAATCTCAATTCATGCTCTTCATCTTTTAG/C/TAGCTGTGGGGTTTGTGTTG TTCTCTGTTTTTGGCTTAGTATCTGACTACTTTTAAATATAAAAGAGATGTATCTAAACAAAAATAG AGATTGTTATCAGAAAGTTCACAACATTTTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ...	---	TTGTGAGGAGTGTGCTGATGCTGCTCCCTCCAGCTCTGCTCCCTAG/C/T/GAACTTCAGGACAACGTGC AG
ESTD-METH	118 C T ...	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTTGGTCTAAGTTGCTGATTACC/C/T/GGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGGTTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ...	---	ATTATCCAGATGAATTTACAAAACCTA/G/TACCAGATCCACAGACTGATATGGCTGGT
ESTD-NFKB1	107 A G ...	---	AACATGGACTTGATATTTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGTGACTTATATCCACACTGCACACTGCCTA/G/GCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATCT GAGAAACTTCTTTAAACCTCACCTTTGTTGGGGTTTTTGGAGAAGGTTATCA
ESTD-NPPA	45 A G ...	---	TGTCCCTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTTCA/G/GTACTGCAAGAGAACACA GACAT
ESTD-NRAS	202 C T ...	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGACTTTTGTGTTGATTATATATAGCAATTTGAGGG ACAAACCATAGAGGAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG C/TIATCCCTGTGGTTTTTAAATAAAAT
ESTD-PAI1	100 A G ...	---	GCCACCAACACCCACCCAGCACACTCCAACTCAGCCAGACAAGGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG/A/GTCAAGCCGTGTATCATCGGAGGCGCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120	A	---	---	CTCTTCAGGAACCAACAGCTCTTCTTACCAAAACACGACTTATTCGTGTCGAGAGGTACAAACCCGTAGA
ESTD- Per/RDS	74	A	G	---	ACTTCTTCTTAAGTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT
EST68308	5	29	C	T	AATCGACTGGCTTTCATAGCTCTGTGAGTGTTCCTTACCTTTCTGTGTTCTAGAACGTTTTCTAG
EST54045	6	39	A	G	GACTGGCAGTTTAAGCTTTCACCTAGGCTTTCGTATACCCATGCC
ESTD-PXMP1	88	A	G	---	ACCTACAGACGTGCTGGATGTGTGTCACCCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG
ESTD-RDS	127	A	---	---	CTGGAGA/GAGCGTGCCGGAGACCTGGAAGGCT
ESTD- s14544	94	G	T	---	GGAAGAGATTAAAGACTTGATTGGAC/CTJAATCTGGTCTTTGAGTGTGGAAGAGTTCATGTC
EST52908	0	45	A	C	TCTGCCCTGAGTTACAACAGAATCCTTTAGTACGCGAGTAATAGATATATTCGACACAGATGGGAAT
EST19590	55	C	T	---	GGAGAAGTAGACTTTAAAGGTAAAGTAGTATTATTTTAA
EST76136	39	C	T	---	GGAATATTAATAATATTTAAATACCTCCATTTTGCTT/GJTCCTTTAGTGAAGATGATACCTGC
ESTD-SPTB	176	C	T	---	AAAAGACATGGCTAAAGTTATGATGTGCATGTGGCAATTTGTTCTTACAAAATCGGATGGGAAA
				---	TCTGTTAAGTAAGTACTGTTTTGCCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
				---	ATGAACATGGTCTTAAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTTAA
				---	ATGCAGAAAGAGGGGAAA/A/GJGAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATAC
				---	AGATTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTAATCTT
				---	CCCGAGGAATCTGAGAGCGAGAGCGAGGCTGGCTGCTGGAGAGAGCGTCCCGAGACCTGGAAAGG
				---	CCCTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGCAACAGGTGGAAGCCGAGGCGCAGACGAGG
				---	CCAGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAACTGAGAAATAGTGCACCT
				---	CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
				---	TTGGGAAGTTAGAGCCTATATTAATACGGAATTAAGGCAGGACACAGAGGCTTAATTGAAAA
				---	TATCCCAAAGTTGAAATGCTCAGTTG/GJCTGTGTGGGTAGATGCAGGATTTATATGATCCGTTA
				---	ACCTCT
				---	ATCACAGGTCTGTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/A/CJTGTTGGTCTGCAAGCCCTT
				---	TGGCAATGTGAGATTGTATG
				---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGAGTGAAGATGTC/JJGGCTCAG
				---	GATGCCGGAAAATGAC
				---	TGAAGCTTCTGCCACGTTGCATTGTTTCTAGGAGAACCC/CJ/JGCGTATACCTTTATCTATAGCCTT
				---	CCCCTAGGTCCT
				---	TGAACACCCCTGTGGTCCGGAGCCAGGTGTGTTTCTCTCTGGAGCCCTGAGGAGTTTGTGTGTGTG
				---	CAGTCCCCCGCCACCTGCTGGTTGAGCCTGGACATACACCTTACCTCCTTTGGCCCCGAGAAAGAC
				---	ATTTACCCAACTGGCCATGTCCCTGGCCTGTGTGTCACA/CJ/JCCTCTGTGAAGACCCCAACCCCTGC
				---	CTCCCCAACCCAAAGCCAGTTTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATCTTAAATGACTTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTTCTCCAGTATGGATGGGATTATGATGGGGG GAGAAAGCAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THFB	125 A C	---	---	TGCGGCTTTCCTCGGAGGTAGACTTCTTACTTGGCTGTGATTTTCCAAAGAGAAGAGTCCCAAG CACACGAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATC/A/C/CTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCA/G/TATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCAATAATATGATGTCGTAA CATGGGTGTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGGATGACA
ESTD-TYR	122 GT	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTCACITTTATACCTTCTTCT AATACAAGCATATGTTAG/A/C/ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTCACITTTATACCTTCTTCT AATACAAGCATATGTTAG/A/C/ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACCAAGTG ACTCTGAGATGTCA/C/T/CAGACTGAGAACCACCGTTATATGTAAGTATCGACAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 CT	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACCAAGTG ACTCTGAGATGTCA/C/T/CAGACTGAGAACCACCGTTATATGTAAGTATCGACAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 CT	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACAC/A/G/TGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACCA GTGACTCTGAGATGTCAAGACTGAGAACCACCGTTATATGTAAGTATCGACAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAAGACAGCCACAGJGJGGCGGGGATGGCGGGGAGTTG TGGTTGGCGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGGGTTGCGATGCTTAAACCTTTGT TTCTGGCCAAAGGAGGGGGGGTCCATGCTGAGATGATAGTGGGOC
ESTD-VWF	36 G ---	---	AGGTAGAAAGCAAGAGTTGATTAGTGAAGGAGAGATGGACCTACCTTCCACACTGTCTCTTTGG TCCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTACGTCAAGCCTCAGCACCAAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGAGCACAGAGATTATTTATCTGAACTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGATCCAG[C/G]TGTGGTGGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
ESTD- TNFAb	152 A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAAGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTACGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCTCAGJGJAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATG CTGTGTGCCCAACTTCCAAATCCCGCCCCCGCGATGG
ESTD- TNFAa	88 A ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAAGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTACGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCTCAGATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGTCCCAACTTCCAAATCCCGCCCCCGCGATGG
EST52418 6	113 A G ---	---	CAATACAGGGTCAACTGCTATGATGTTTGGAGCCAGTCAACCTTTGTGGCTACAAGATGTGG GGGAGTGGCGGGAGTTGGCGGAGTACGGGCTGCAGGCATACACTJAGJAAGTGAAAACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCJAGJGGGCTGGCTTATAGCCTCCAGCCAGCCAGTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAACTGGGGCCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGTCAACTCTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAAGJATJCTCTCTC CTCCCTGAGTGGAGCAACAGCAGGAAACAGCAGGAGGAGCAGCAGGAGGAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCAAATGATTTCACAGTGTCTATCTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTACCAATTTCCACAGTGGT CCCJGJTAAACATTTCTATGAGCCAGGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTG TCCCAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	---	AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTTCCTGGATCTCCATGGGCCAGC[C/T]AGCA CTGGTCCCTGTAGTCTGTATCAGGTAGAGGAGATGGGACCAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGACAGATATTAAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	---	CGGTCTCCTTCCAGGTATTGTTCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCGATCCATAAG GCATTCTTGAGGTGAGTACACCTTCCCACTCTT[C/G]GAGTACAGAAAGGAGATGCGATGAACA GCAGGAACACGTGGAAGGCCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	---	ACCTGGTGTGCTGGTGAACCTGGTCTCTGGCATGGCCGCCCTCTGCGGCCCTGCGGCCCTGG TCCTCTGGTGTGGGTAGTCTCTGGAGTCAACGGTCTCTT[G/G]GTGAAGCTGGTCTGATGGCA ACCTGGGAACGATGGTCCCCAGGTCCGATGGTCAACCCGGACACAGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	---	AGTGACTTCCAAGGAATGGCTACCCAACTTGCCTTCATGCGCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTCATACATGGATGAGGAGACTGG[C/A]AACCTGAAAA AGGCTGTCTATTACAGGGCTCTAATGATGTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTGTAGATGGCTCTCTAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCCTGTCACTT[C/A]G/GGGTGTTCAGGTGGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGGTGGACCTGGAAACA[C/T]TGGACTCTTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAAGATATACAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	---	GCCGCAATGCCGGAGTTTCTCCAATGTGTGGAGAGGCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCCTCCTCATCATGAAAC TGGGAGGCCGGCAT[C/G]GTGCTCATGCTGTAAATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT CACTTGAGGTGAGGATTTGAGACCAACCTGGCCAAAT
EST12274 0	135 A G ---	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTTCTGCTTCCAATAGAGCCTTACCAAGGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTG[C A/G]TAGTAAATGACCGATGGGGTCAGAACTGTCTCTGTCACCATGGAGGATATACTAAGTGAAGA TAAATCAAGCCACAGAGCTTGCAGATC
EST76807	91 G ---	---	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTAGCCGATGTCTCTATCTCCAGCGGCCCTGTCATC CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCGGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

WI-2625	98 G A ---	---	---	---	GGCAGTCTGGCTGTAGTGGTAGACAGCACTGAAGGATGGAGGAAGAGAGAAAGAAACAGGCAGAA GCACTGTGGTAGTTAACAAAGGCTTATTAGGA[G/A]CAAAATTGATGATACCTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCCA GCCAGCAAAAG
WI-2924	54 G A TAGG	---	---	---	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG[G/A]ACCCCTGTGATT ACACTTAGGGCCTACCTGGATTATTAGAACAAATC
WI-2939	72 G T GTGCCITT	---	---	---	CCATTGTTGAGGTTGGTGGGTCACTTGTCATTCCCTCGCACTCAACAAGTGGCTGTCTCAAGTGC CTTT[G/C]CAAGACCTCCCTCAACAAGAATGCTTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT TTATCCTGAAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCCTG
WI-3203	99 G A AGACGAG	---	---	---	CTTGCTACCATGCATTTACAGCATACAACCCCTCAGTGAATGCCGTAAACCCCATTAATAAACAT CTTGCCATCGAAGGGTTATGCCGCAGACGAG[G/A]CCACACAAGGCAATACTTGAAGTCACTTGGGA GAATAAAGATTTTGGATGGATGAAAGCAGAGAAGGAGATGCTAAAAGTGA
WI-3473	101 A G GCCCTAGGGA	---	---	---	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTGATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[G/G]TAGAAAATGTTGGTGACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAA[A/G]TCAGGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTGGCTCCCC
WI-1796b	29 A G ---	---	---	---	ACACACTTTCTGTATGCTCTTCATCAA[A/G]TCAGGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTGGCTCCCC
WI-1796	29 A G ---	---	---	---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAAGAAAGATGGGGTGAGT AGTCACATTAGGTATTTTCCAAATAA[C/T]AAAAATGCCTCTGAAAAATATCTCTCCCATGTCCTCTGTC TAAATAACATTTTCCC
WI-4360	93 C T AAATAA	---	---	---	GCTGAGCTTTGTGGCAGAGCCAGGACAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAA CAGGAACCCAAAATCAGTC[C/T]GGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87 C T ---	---	---	---	GTTGTGCCCTGTAGCAGACACAGAAGGCA[G/G]AGAGGAAAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ---	---	---	---	CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAAATTGTATCTGTTCTACAAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATTACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTACTAGGTGCCTATAAATAGC
WI-1980b	140 C T ---	---	---	---	

WI-2015b	190 A G TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAAATATACAAATTACTTGCAGATAGCATGACCATGCTAGTGAAACCCACACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATATAAACTCTACATGGTGTCTTTTCCAACTTAA/GJCATATACTT CTAATACCATAGAG
WI-754b	49 C T GAAGGCACAGGAGAGATGGCTGTCTATCTACCAGCCAGGAGAGAGAGC/TJACATTTATTGGTAA TCCTATAAGTGCATCTTTAAATTTGATTTACTTTAGA
WI-754	22 T C GAAGGCACAGGAGAGATGGCT/GJGTCTATCTACCAGCCAGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAGTGCATCTTTAAATTTGATTTACTTTAGA
WIR-1b	56 A G AGGCAATCAGACCTACAGAGAGGAAACCCCAATAAAACTCTGATGATCGTACATCC/A/GJTGGCGCTG GAGGGTGATGGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G AGGCAATCAGACCTACAGAGAGGAAACCCCAATAAAACTCTGATGATCGTACATCC/A/GJTGGCGCTG GAGGGTGATGGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G TAATTTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT/A/GJTCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T TAATTTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA/A/TGTATCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C CGGGACAGAGAGACAGAGAGAGAGATTCTGCAGCATTCAACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5f	196 C CGGGACAGAGAGACAGAGAGAGAGATTCTGCAGCATTCAACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5e	194 C CGGGACAGAGAGACAGAGAGAGAGATTCTGCAGCATTCAACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG

WIR-5d	191 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5c	177 C ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5b	159 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACAC AGTTTACGTCCAG
WIR-5a	37 A G ---	---	TAACCTGAAACTTTGCTTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGGTTGGGCGAG
WIR-6	63 A C ---	---	TTTCGTGACTATT[C]/AAGCATCTGTAGAATATTGAATACATAGCTTGAGATTGATC
WIR-7	12 C T ---	---	GGCGTCCTATGACTATCCTGGTCATTGATTGACTAATGATTCCTG[C]/TGCCCTTG
WIR-8	46 C T ---	---	AAACAGAAAAATAGAGGTTAT AAGGATGGAACATAAAAGTTGTCAGAAGAGGATGA[C]/GJCTGAAG AAAGAAATTACTCCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WIR-2	56 C G ---	---	TGTCCTTGCTTATGCCTGCTCTTTCGCTTGGCAGGATGATGCTGCTATTAGTATTTACAAGAAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G]/ATCAGATCTATCTTGTCATCCCAACGTTTTACATAAAA TAAGAGATCCTTTAGTGCAACCCAGTGAATGACATTAGCAGCATCTTTAACACAGCCGTTGTGTTCAAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACTGTTCTCACTC
WI-7069	93 G A ---	---	GGTCATTTCCTTTTATCTGTCAGGCAGCCAGCTGACTT[A]/JCTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTACCCTGATGATTATACCAATAATACAGTTCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A T ---	---	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC[A]/GJTATTTGCAAGCAGCAATACAAAAAGTA TTCATGAAGAATGCATAATCTCTGAAATATGAAACATCCCT
WI-18612	37 A G TGC	CCTATATTCA AGTTTGGAAA CTTGCAAT	TTGTATTGCTG CTTGCAAT

WI-18517	87	C T	CAGGAATCAG GTGCAACA	TGTTTGGACAA GTGCAACA	TTAAATACTAACTAGGGCTCACCCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGAC/TTTGTTGCACCTTGTCCTCAACACCACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA GC	GCTAAATTAAA CTGCACCTTTT GC	CGATTGACAACCTTTTATTTCACCTTAGGTAAACAGTCCAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA/C/TTAGCAAAAAGTGCAGTTTAATTAGCAAAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C A	GCTGCTACTCT AGCATCTGGA T C A	CCCTCTGAATA TACAACGGAGC TGAAGGCCCTG CTGG	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTTAGC ATCTGGAAT/C/GCTCCGTTGTATATCAGGAGGGGA CACCCAGGCTGTACCCAGGCTTCTGTGCGAGCACACCAAGGGCAGGTGGGCTTGAAGGAGCC CTTGAGGAACACGGGTTCTCCGAGGGGTAC/C/CCAGCAGGGCTTCAGCTTAAAGTCG
WI-18704	99	A C	GGTTCCTCGA GGGGTAC	---	TGTGGGCAACCTTGTTTTAAATTGCAAAAC/A/GJACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18673	29	A G	---	---	ACCAGTCATGTTTATTGGAGGTTAATTCCTATTAGGATATGAAAGGATTGAGCAACGATTGAGATT GTGTTCTCAGCGAGGGGCTCGGGCCAGGTCGTGGGGTGGGGGGTGCAGAGT/C/GTGTCTCTTC AGTGGTATTGCGGACC
WI-18640	121	T C	GTOGTGGGGT GGGG	GCAATACCAC TGAAGAGGAC A	GGGGAGGAGGAGTAGATTGCCAAATGAGGCAATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTTCATCTAAT/C/TTACTGAAGCCATTTCTTTGGTTAACTTAGA GGGAGAGGAGGAGTAGATTGCCAAATGAGGCAATTTTTTAACTCCCGAGATTTCTT/GJCTTTA TTTTATTTTCATTTTCATCTAATTTACTGAAGCCATTTCTTTGGTTAACTTAGA
D11734	83	A C	TCATCTGATAC CTTGTTCCAGAT TTC	AACCAGGATA AGGCTACAACT ATTT	GAGCATATGCTGCATGAGGACCCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCTATGATA CCTTGTTCCAGATTT/C/AAATAGTTGTAGCCCTTATCCTGGTTTACAGATGTGAAACTTT CAGGACTTGTGGTGACGCTGCAGACACAGAGCACAGCTCATGGCAACATCACTGGGGCCAGAGAG AGCTGCCGCCAGTGCATCATTAGGGGGTCTTTCATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT/A/TCCTGGCCTGAAAGTGGCCCATCATACCCCACTGTT CT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGOC AGGGC	TAITTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT/C/CTCATCCATACCACTGCTGATTG
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TAITTTGGCTCACTCTGGAGGCTG/A/GAAGCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGGAGTGCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A
EST10052 2	24	G A	GCTCACTTCTG GAGGCTG	TGTTGGAACCTC AATCTTAGACT TC	CTGTTGAGTCAATAACCTGGTGGAGTGCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

EST10605 2	118 C G ...			CTTGGTAAATCACAGTTCTGTATTATACAAAAAATTTGTTTCTCTGACAAAATGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G ...	CTCTCAAGTAG ATAAGAGGCA TAATCT	GCTAAATTTTC AGAAAGATT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/JAA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAACCCAGAGAGGAGCAC
EST11260 8	101 G T ...			TATGGAGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGAAATGAAGTGTCACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ...			TTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCACAGTAGATTCTTTGGACGAAGAAAATCCT TCTGTGGAATTCAGCTTACCGCCCTTCCCTCATCTGCTGGTG[C/T]TCCCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G ...	CCAACCTACTT TGGAGCCCT	TCCAGCTTTCT CTAAAACTCC T	GAATCTGGGTATTAAATAGCGGGTGCCACAGGACACATAGGAAGAGCATCCCAACCTACTTTGGAG CCCT[AG/JAGGAGTTT]TAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGAA
EST11772 6	74 A G ...			CCAGGAATAAAAGAAAAAGAGTCAGAGGAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[AG/G]GACTATTTTCACTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ...			CTTGCCATTTATTTTGTGCATGTGTTCTTAAAGGCTGTGAAAGATAAATTTGGAATGTGGGAAC ACATAGATCCCAGA[G/A]TATTAAAGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42 G A ...	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAAATTC ATGAAGTAAATTCATTATACCAAAAAAGCCCTCCACAGAACTTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56 A G ...	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCTGGAT	GCCTAGTAATCCAAAAGGAACATGTTTGATAATAAACAACCTCAGTACAAAAGTCGT[G/J]ATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC
EST12055 9	32 T C ...			GTGGAAAATTTTATCTGTACGCTCTTCCIT/CJATTATAATTATCTTGTCCCTTGATTTCAGCACCC CACCGAATTTGCAGGCAGTGCTTTCTAAACTGTGCCCTGTGAGCTGTAAAAGTCTTCT
EST12492 1b	95 A G ...			CCCCTAGCAATGACTTGGAGTTGTGTCCTCAATTACCAAGTTACATACTGTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[G/J]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G ...			ATCTTGAGGTTTCTGGCCCTGTGAG[G/J]AAGTGACATCTTTTACTTACCAGGTCAGGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTAAAGGGCTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATAACTAGGGAGAAACCAAACTGGAGGCAAGTCCACAGGTCCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGTTTCGATGAAGAGAAATGCTCACGGGGAATGACCATTTTTTAAGGGCCATGTG GTCGCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAAATGATCGGTAAAAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAATGACAGTGTGCCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCCTTCATTATTATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGC[A /G]TTGAGAATACAATAATTGAAGAAGAGTCACTGCCTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGGTTCTCCAGGATTCAG[C/A]CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTCTTGGGAGTGACCGGATGGGAATCCATGTGTCTTTCGTACTCCATCAGGTCAATTGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCAGTTATTTCCACCAGAAATTTGTTGCGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACCTGTTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAACAACAC[A/G]TCTGTCACCTG CAGAGACCCACAGGGACACACATTTCTCTCCTCCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTTCTTAAATGAAGCATAATAAACAGTTAAAAATCTCAGAAAAATCATCTATAGTTGA GTGTAACAACTCCCTAAATCAGTCTTCTAGGGCCAC[A/C]TGGAGCAGAAAGCAGCTTCCCACCCAAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTAAAAATTTAATCGCTTTTATACAAATTGACACCAATAAAATGCAC[A /G]TATTTAAAGTTTACAAATTTGAGAAGCTGACACGTTGCCATACAGACACACCTCAITTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGCGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGCTTATTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATAATGAAATAGTCT GGCCATT[T/G]GACTAACCAAGTTCTACAAATTTACATAATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAAACATG
EST13230 6	72 G A AGAGAGC	GCTCAGATGTG ACAGAGC	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTACAACCAACTGCGGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGCTACTGCTTCAATCCCTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAAGATTT TGACAAAAAGA G	ACAAGAGGGTT TGACAAAAAGA G	AAAGATATAAAACAACCTCCCATCAGTAGCAATACAAGGTATACATTTTAAACCAGATTTTCTCAGG CCTT[C/T]TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCTCTTGTATATAACCA

EST13278 2a	51	A G G	CITTCACGAA CAATATTTTAG	CATATCTGG GTGGTGAGAA	TTGCGAGAACGTTTTACAGCTCCAAACCTTTACCCGAACAATATTTTGGGAGATTTTGAATATAT TTCTGTAGTTCTCACCACCCCAAGATATGACAGCTTG
EST13282 0	99	A T	CCACACATTTTC AGTCCAGA	GATGGAAATTT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAAATATTAGATAATACCTGTTGGGAAAGTGCTGAATTTACTAGCC TGCCTGAGAAATCCACACATTTTCCAGTCCAAAGATTAACCTTCTCAAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39	A G CTT	CAATTTT TAGA AGTTGGGTTT	AAATCACTTCA TGGAAATTTCA	AGCTCATCTGCAAGCAAATTTTAGAAGTTTGGGTTTCTT[AG]CTGAAATTTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTTACGTTACTTAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGTGGGCTTTTIG
EST13518 2	45	C G ---		---	GAAACATCCTCCAGTAGATTGAGGTTAAAAATGATTCAGCATTTA[C/G]ACTTTAAAAATTTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG
EST13522 8a	66	A G ---		---	CAGGTTGGTATTCTCAACTAGGAGCTATTTGCCCCCATCCCCCAGCGGAGTGCTGGAGAC[A/ G]GTTTATTGTCACAACCTCGAGAGGTTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69	T C ---		---	CTTAAAGGAAGTGAGCCAGATGAATCCATGACCAACCTGGTTGAGAGGCCATTGGTCTAGGAGTAGA AA[C/G]GCACACAAGGAATAAGGGAGAGGAGGTTGCGTTAGTTGAGGGAGAGAAAGTTGGGAAGCA TTTCAAGCTAAGTAATGGT
EST13785 0	101	C G ---		---	AAGATTACGGGACCATAAGAACTGCCCCCGACCCCATACACACACAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAGTAATGACTTTCTTGAACAAA[C/G]GATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A G ---		---	CCTCAACCATCTGTAAACCCGAGCCC[AG]CAGTGACCCGGGACTTGCTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23	A G ---		---	CAATGGTGTCATGTGAACATAT[AG]ACCTATTCAATAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	42	T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT	AATATCAATGCATCTTGTGGCATGCTAGACAGAGGCATTAT[C]TTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCTCCCTTCACACTCATTTTAAATGT
EST14812 2	50	A G A T A	CAAGTCAGCTT CTACATCTGA	TAAAGATTAG TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTCTGAATA[AG]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCGGAGTTGCGCTTTCTAACATTTTCATATCAGGTGAAACAAAT TTTTTCATATGGGTGATT
EST14815 3	128	A T A T A C T G G T T	CATCACCCACC ATACTGGTT	CGGGAACA GTACCGAA	TTTGGCTCGGCAATACATAGTGGCAATGCAGCGGTGAGTTCGGCCGCTCCCCACTGAACCCAGTAAT TCACCAGACATGGCGCACTTAAATAAAGTTGCCGTCATACCCCATCATACTGGTT[AT]TTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A	TTTAAACCCCAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCGCTATAGCTTGGATATCTTA ATCTCCCCCTTTGTCATATAATCATATAGCAAGGGACTC/AJGGAAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GTCACCAGCACCTTTTATTAGACGTGAAAGACAAAAGACAAACAGAGGA/G/CJAGCAGAGAAATAATA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC/G/AJTTATAG GGAATAATGAAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAATGGCTCCCAAGGT
WI-16782	96 C T CACTGTAAGG	CTTCTCCTTCTAGACGTGGAATACACACGGAATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAGGA/C/TJGATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATGTGGGG
WI-16783	64 A G G	AAAAATGTAAAACCTTAGAGGTGGCTCTTTTGTGTCACCTTTTCTGAGATGTCCTTTTACCTGAG/A/GJ CTAATAAGGATTGAACCAAGCAGTATTTTTTAATGGCAAAAGTCAGATGTAACCTCGAGT
EST15948 2	58 T C	CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTTAACTAAAGTCAAGGCAACATAGGA/T/CJTGTA CAGCACCACTCGGACCAGGAAGTGTGAAATCGTCACACTAGCTGCCAGCCCTTTTTCCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89 G C	GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAAGAGCTGTTTGTGACGCC TTTTCCAGAAAAGGCCGCTC/G/CJGGGTTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T	CGTCTGAAGTTTTCTTTATCACAAATCACATCAATCCCTCGGGCCCTGCTCAAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTC/C/TJAAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G	ATCCAGCTGTGAAGGACAGGAG/C/GJGTAACACAGTCCATTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTGGCTC
EST16104 9a	83 A G	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTATTGCAG CTGGTTCTCCAGGGA/A/GJTTGGCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C	ATGGTATAACAAAATCAGTTCAGGTTTTTTTCTGAACAAATGATCCTTTGGCTTTCCCGTGGCATG CTCCTAAACAACTAAACAACCCCTCTACGCTAATCAGTCACCTAAGATA/T/CJGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G	ATGGTATAACAAAATCAGTTCAGGTTTTTTTCTGAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCCTAAACAACTAAACAACCCCTCTACGCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ...			AGCCAATTCAAACGAACTCTATCAAACACACAAAGGCCTAGAGGAGATT[C/T]AATGAACGT AAATAATCAAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTGTATAGGA
EST16182 6	54 G A ...			CATTGGTTGGGTAGGGAAGATAGTAGTGCAAAATAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTAGGGTGATAGGCAGAAAGTAGTA
EST16183 2b				GCAGGTAACACTGTGGTTCAACACGATTTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGCTTCCTGGCCCTTCCTCGTTTCATATTTTATGTCACTGTCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ...			AATCTTAGGCTCTGGCTTTCAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAAGTCAGCATCATAAACCACATGGGTGCACATGCTCACGCACATGGGTGC
EST16229 2c	52 T C ...			TGTGAACCTCGAATTCGCTTGCCAAAGTCTGAGTCACAGTTTCATTTGGGAG[T/C]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCCACTAGCTGATTCAGACAGGAGGCTGCA
EST16229 2b	45 T C ...			TGTGAACCTCGAATTCGCTTGCCAAAGTCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCCACTAGCTGATTCAGACAGGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTCTCACACCTCATTTGGCTGGAACTGGGTGCACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGGTGCATCAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ...			GCCACTCTCTGTGGCTTGTCTCTGTCCAGCTGCTGCCAGTGCCAC[A/G]TGGTCTAGCCTCATGG CAGAAGCATTTTAGCCAACTCCTGGTGTCTCCACTCTCTCTCTTCCGCCGCTGGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ...			GTACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	TTCTTCATAAG	GTACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT[C/G]TTCATTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ...			TTGCTTTTATTATCCAGAACGGCATGCTACAGATACITGIACAGCATGAACATTTTATTATTACAAA AATGGCTTCCAAACCATTAAAATGAACCTT[C/G]GAATAAGAGCATAAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAAACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTACAAAGACCTGTGCTTCAAATTGTTTTCCTGATAATGTGGAGAAATCTGCTCTTTATGTA

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WI-16879	79 C T	GATACAGGCC ATATTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACAACTCTCTAGGGATAAAGATATAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTTGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAAATGCCA CGTCTCTGAC	GACACATGTC GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAGACAATCTCCCCCTTTACCCCAAAGGTTACTCTGAC AAGGCTATGAATGAATGCCACGCTCTGAC/C/GCGGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAATGTTTCACTACCCGGGGAGAGCAAGAACCACTGGAACGGTAGCTAACTTTGGGCAGG TTC/G/A/TTAAATTTGGTCAATTCAGAACATCCAAAT
WI-16905	75 C T	ACTTGGCCTGT GTTGTTCA	GTCATATCTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA/C/TCCCACTGGCTAGAGAGTATAGACA
WI-16910	74 G A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAGAGTAAGATGGCG CTAGAA/G/A/GTATCTGTTATAGAAACGATACITTCATTTTGGGCTGAACCAAGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAATACTACCACCTCTCTGCTACCACAGAGCCTAAATCTAGGAATTTGAC TTTACTGCAGCCATTACACCAGCAC/C/TGATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGG/C/JCCA CGGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAG/C/GJACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTGTTTTACTTTAAATGCACACTACATAACAACCTAATAT/C/JCTTAACTTGGTCCAACATATTT AGTATAACTAATATGAGTTTTTATAGTAACTTGCAATGCCATTAAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGGCGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATTT/CJACGGCTGG AAATCAACATGGCTCTCTCTCTGTGAAGTTGTACGATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60 T G	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTGCGCCCTCATCTGAGATT/GJGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46 G A	AAGCACCCAG AAGTACACTG TC	CACATTCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTG/C/AJCCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23 T C	TTCACAGGA	AATAATACGGT	ATGTTTCAACAGGAAAGCCATGTCATGACATTCAAAACACCGGTATTATTAGAAGCTCATTTAAT
EST17127	74 C T	CACTCGGCAC	GGGAGGCGAGG	TGTTTAATGCAGACAAAAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA
9b		AGACAGAGT	GGTG	GGTCCACG
WI-17040	94 T C A	AATCTCTTAT	GGACTATGGCT	ATTCCGCTCCAAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA
		CATCTCAAGGC	TATTCAGTGAT	CAGAGTCCTGGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTTCTTAAGTAACAAC
			G	CACGCGTTTCATTAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
				GAGAAATCTCTTATCATCTCAAGCCAGTCATCATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTC
				AAATCTTCTCATATTGT
		GCCAAGGGAT		TTGTTTGTGTTTGTCTCTCTCTGCGCAAGGATTAACGTATAGGTCCTTAAACAAGGGGATC
WI-17044	47 G T	TAACGTATAG	GGGGATCCCT	CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACCTGACTCTCTCTGCAGAAATGGCAGGGAATCGAAT
		G	TGTTTAAGA	CAAAAAGAAAAGCAAGTG
		TGGACTTGTCA		GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGAAGTGTGCAGCCTATAACTACTCTTAAAG
WI-17021	62 T A	GCCTATAACT	TGTAGAGTTAG	CAGCTGCCACTAATCTACAGGCACAGTAACACTTATACAGGAGCAGCATGCCAAAAGTGCCCTGG
		ACTC	TGGCAGCTGC	GAGGTGCCAATAAAATCAA
		CCAGAAAGGA		
WI-17065	90 T C	AAAGCATAAA	CCCAAGAGAC	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCGTATCAACATGTGCTGTTTCTACTTCCGGTA
		CTT	AATGAAATCCT	CCAGAAAGGAAAGCATAAACTTTCAGGATTTCATGCTCTCTTGGGT
		TGTACAGCCA	GAGATGTTGAA	
WI-17066	32 A C T	ACATCACTGTT	AATGTTCTGGA	TTCATAAGGTTGTACAGCCCAACATCACTGTTTCATCCAGAACATTTTCAACATCTCAAAAAGA
			A	AACTCTGCACCCATTAGCAGTCAATCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T G	---	---	TGCTGACTGTGATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAGCAT
WI-17104b	108 T C	---	---	AACTCTCTACACAGGCCCTTGGCTACATAGGAGTATATTTGGCCCAAGACTCACCCTAGAAAGTATT
				CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTGCGAGCTTTCCCATTCATTCCA
				AATCAGAAAGCAGTCAGTGGCCCGGTGTTCCAGACGGCTTTCCTCTTTGTTAAGAAATTA
WI-17114a	37 T C	TTCCATCAAG	TTGTATTATAA	AGCGTCCAACAGAGATGTTCCATCAAGGACTTTGTTTTCCTCTCTCTCACTCTGCTATTATAATAG
		GACTTTGTTT	ATAGCAGAGTG	AAGCTACCTCCCAAGGCCAGATGCTTAAGTGCTAAAAGAAAGACTGCAGCCACAATCAGAGTTACAT
		GATGAAATTC	AAGAGAC	GGGA
WI-17150	76 T G	AGATAGTCTTC	TTCTCAGAATC	
		CTCTT	CTGGAAGATAT	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC
			G	TTCTCTCTTTCATATCTCCAGGATTCAGAAAGGCCCTCTTGTGCTCTAATTT
		CATTTCTTTGT		GAAATCGAATACGTCCTCTTTTGTAAAAAACAATAACGTTTAAAGGCAAAAGCAAGATTCTG
		AAAATAACAA	CAGAATCTTGC	TAAACCAACATTTGGAAGGGGACACAGGGAGGGGAGGAAAGGCCAGATTTTCAACGGTTT
WI-17163	43 A G	TAACGTT	TTTGGCCT	CTCCACATCTGCAGACAAA

WI-17178	127 T C	GGACTCOCTCA	CCCTCAATTTT	AGCAATGTCCCTCCCAATTTTCATTAGCTATGATGGAGTTATCAGTTTCATTTCAGAGCGAATTACTGG
WI-17180b	81 C G	---	CAACTGCTTC	GGCAGGGGGTTTAAATATCCTGATGGGTTTAAATCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180a	47 T C	CACAAAATA TAGAGAATCC	---	GCAGTTGAAATGAGGG
WI-17180a	47 T C	TGCA	TGCGACGAGAC	TCATGGACATCCTGAAGCAGACACACAAAATATAGAGATCCTGCACATTCCTCCAGTCTCGTCGACAG
WI-17156	54 G C	TGTTCTCTAAA CTTTAGATATC	TTGGG	GCTTCAACAAATTAC[C/G]AACATCTTGCCCATTTTGTTTCATTATCCGCCACCCACACTGACAGATGAG
WI-17149b	79 T C	---	CAAGAAATAT	GGAGTC
WI-17149a	48 C G	CAAGGTTGA AGGAGGAACA	ATATTTGATTC	TCATGGACATCCTGAAGCAGACACACAAAATATAGAGATCCTGCACATTCCTCCAGTCTCGTCGCA
WI-17197	67 G A	CTGGGGTAC	TGTGGAA	CAGGCTTCAACAATACCAACATCTTGCCCATTTTGTTTCATTATCCGCCACCCACACTGACAGATGAG
WI-17198	38 A C	GCAGAAAGTAG	---	GGAGTC
EST18753	27 C T	CTACCCAGGCT	CCACGCACGTG	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTTAGATATCTCCCATTCCTCCACAGA
WI-17108b	74 C T	GGTCTCAT	CATGA	ATCAATATATATTTCTTGGTTGGAAATTTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT
EST19067	41 A G	GGTCTCAT	ACTGAGAAAT	TAATATCTTG
EST19067	40 A C	CGTACCATTT	GGTGGTGGT	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATCTCATGCGAGTGGGTGAA
EST19125	28 A G	AAGGTATAG	GCATACC	ACCCAATTGTCATTC/GTGTATGAACACTACAAAAGGATGGGGAAGAAACACATTTCTCTCACA
EST19125	28 A G	TTT	CCATACC	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATTC/GTGTATGCACGTGCGTG
EST19125	28 A G	TTT	CCATACC	GAAACCCAAATTTGTCATGTGTATGAACACTACAAAAGGATGGGGAAGAAACACATTTCTCTCACA
EST19125	28 A G	TTT	CCATACC	ATTTTGCTATGTTCCCTGGGCTGGACTCCAGCAATCTCTCTGCCTCAGCAGAAAGTAGCTGGGGTACIG
EST19125	28 A G	TTT	CCATACC	/AIGGTATGCACCACCCCTCACCCTGCTTATCAGTTTCGTTTAAATAGAAATATTTGACTTTTAGATGCGCA
EST19125	28 A G	TTT	CCATACC	TGATTTTCAGTACTTTTCTCCCTGCTGCTAGTTTAC/TAAATTTCTCAGTGGACAAATGGACAA
EST19125	28 A G	TTT	CCATACC	ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGACACATCC
EST19125	28 A G	TTT	CCATACC	TTC
EST19125	28 A G	TTT	CCATACC	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGCGATCCTCTGCTCTGCAGTGGCTGG
EST19125	28 A G	TTT	CCATACC	GATAAGACACAACTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCTGATGGTGGG
EST19125	28 A G	TTT	CCATACC	TTATTTTAAACATAACACAGATGCACCTTGGTTTTTACATTTCTCTGGTTGCCATTCAGTCTCAAAGT
EST19125	28 A G	TTT	CCATACC	AAACAC/C/TGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCATTACAGAGT
EST19125	28 A G	TTT	CCATACC	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/GJGTGGCATTAGTACATTCAACT
EST19125	28 A G	TTT	CCATACC	TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT
EST19125	28 A G	TTT	CCATACC	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JAGTGGCATTAAAGTACATTCAACT
EST19125	28 A G	TTT	CCATACC	TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT
EST19125	28 A G	TTT	CCATACC	CTGTTTCTCAGAGATGACACTGCCAACAA/GJTCACAGATTTTGACATACAAATACAGTTATGTTATGGC
EST19125	28 A G	TTT	CCATACC	TATTCACAAATTTACAGTAGTGTGTTTTTCTCTCGAAAAA

EST20824 8	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGAAGCCGGAGTTTATTATTATTTCAATCAGTCTCTGTAATACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGT/GTJCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCTA	TTGGTTAAATGATGCCAGATGGGTACATCCTCAGAACTTCTCAGCCT/GAGJGTAGCACAAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128 G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTC AGAAAGCAT	TGATTGGGCTCTGGGAGCAGGTGGGCAGTTCAGTGAGGAGCAGAGGAAAGTAGACGAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTCTGAACACCTGCC
EST22111 3	82 T C	GAAGATCTGT CTGGCATTCTT	TGGAATAACA GCCCCAC	CAACAAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTCTTTT/CJGTGGGGCTGTTTTTCCAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCAACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATATTCTGCT ATTCTGCCATJ/CJACCGCATCCTTCATGGTAGAGTATCAAGTAAAGTTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACACTGTAAACAG TAGCATTCAATGGTTTTTTTACTCTA/JTGTCAAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA CACTTTCATCATTCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCC/A/GJCCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA CACTTTCATCATTCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAAT/JCJACATAAAAAATCCACCACACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA CACTTTCATCATTCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGC/A/CJACCAAGGGACGTGTGCCAGGGCCACCGTGCAGGCAAGTG GTCCAACTCCTTCCCTCCCTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGGCTTCT TAAGCCTTTTTTAACGT
EST22433 c	103 A G	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAAGTGACAGA	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC/A/GJCTGTGTCAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAAGAAAAAATGACTTAAAAAATACAATTTCTATCCAGAAAAATGGATCCTTATCTG CACA/A/GJCCATTGAAGAAAAAATTTATCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCC	TGCTGTAA TTGACTGTAA TG	GCCTTTTATTGTCCTTTTAAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTACCCCA ATT/CJ/CATTACAGTCAAAATTACAGGCAATATAATAGGCTAACAGAATGCTTGCAATTT
EST23021 0	108 T A	---	---	TTATTTCTCAGCTTACCATTGTTGTTACTTATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTATCTTTGCCTTT/AJATGGTTTTGACAGTTTGTGCTTTCT T
WI-17387	55 C G	CCTTGCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTOC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAGCTCCAGAGGCAG/CJ/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G TT	GGCTGTTAGTT TTGTTTGT	TGCACCTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTTGTTTTTCCCTT/GJ/ATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGGCGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCGTCOCG CCAG	CCAGTGACGAG GOOGA	CTGACACGTCCTGTGTGCGGGGTGTCATGTGGGTGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGGCTCGTCACTGGCCCTTGGTCACTTTGTATTTCTGCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAATGCATTGTTGTCCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCAATAG
EST25356 3b	95 C G	---	---	TCCTTGATACAGGTAACCCAGTTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/CJ/ATAATGTCAACATCAGGATTCTTTTTT
EST25356 3a	26 A C	---	---	TCCTTGATACAGGTAACCCAGTTTTGT/A/CJACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTCTTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJ/TTAGGCGCAATTTACATTGACGGTCAATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGATAA	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATCAACATT ACTACCAGTTATTGATAA/T/CJ/GATAGAACCCAACTAGGCGCAATTTACATTGACGGTCAATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CATCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGTTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCCCTACT TCCTTGTTGATAAACTCC/CJ/GJATTTGTCGATTCTAGCTATAAGAAITGGGGCCACTAAGTGGGTC

WI-17623	46 T C ---			---	TGTGTTTTAAATTTCCATATAATTAATGTTGGGCACATTTC/GCATGTGCTTACTGGGTC ATTACATATATCTTTTGTGAAGCATCTGCTCCAAATCTTTTGGCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ---			---	ATTTACACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGATTC/GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGACAGAGAAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC		CAAGAAGTTTG GACTGCC	ATTTACACAGAGATACAAAGGCAACTATGTGCAGC/AJACAATCTGATGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGACAGAGAAATG
EST26780 5	69 G C ---			---	TCAGCTTTAATTTAAGGGACATGTAATAAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTCTGTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---			---	TACTTCAGTTTAAGGCAATTTCCACACAGAGACTGTCTC/JAG/GAGACGGGCACAGAACCCAGACACC GTAGAAACACCAACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---			---	CAAAGGATTTTATTTTGTCCCTAAAAGTAAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCTC/JTTTACATGGGTGACACATCTTTTACATGACACAT CATCGGAAAACAGACTGA
EST27504 0a	33 G A ATT	GCATTTGCAA CAATTTAATA		GCTGGTGTGAT GCTACTGTAAT G	TTTTTGACATTTTGCAACAATTTAATAATTTATC/GA/CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTCAGTATTTCTGTTACACATCTGTTAAACAAGAACCCATACATT GGTAAATTCATCT
EST27662 4	51 C T C	CACATTTCTGTT CTCCAGTCTTG C		TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTTCTCCAGTCTTG/C/JAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACACTCTTTTGGAAATGTTT
EST27788 3	100 A G ---			---	ATTTTATTAGGCGGTACAATTTCCAAGGTGTAAGGTGAAGGAAAGGCGAAGGCGGCAATACAT TATTGAGCTGAAAACAACATTTACATTTCAAGGAC/JAG/GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC		GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAACTTTCTTCTGTGTGGATCCAGTGACGTGGAAGTCATCAGAACCCCACTG/JGTACTT GGAGTACCTCTCTGCAACAAGATAGCTGGCTGATTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAAATTC AATCTGTAC		TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/GA/JAAATG GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---			---	TCCCGCTTCCAAAGCTTTATTGGCAATATGCTCTAT/T/CJAAAGAATGATCAATCCTGTTGCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACACCCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTCTCGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTTCTTCTTTAAATATATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACACAGACAGAGACATGAGTTTCTGACTGTGACACATTGGTGAAA
WI-17724	50 T C	TGGGCGCTCC TGTC	TGGTTGGCAG TGTC	AGAAITGGTCTAGTAATCGTTACAGGATTCGGTGATGGGCCCTCCCTGTC[T/C]GGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGGAGAAAGACACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGATACACTG TT[C/C]CACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTC
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT CATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACACAGAAAGTGAAGTGCTATT[C/C]GTTACATCATACCAAGTGATACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTC
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAACACACATTAAGCATCATTTGTCAC[T/G]AGCTAACTCCT CAAATCAACAATACCCCTTTATTTTAGCCATGAAAAC
EST29128 4	58 A G	---	---	CTTTAGAGGACACCACTGTTGTTGGACTTAGGGCTACCCCTATTCAGCAGGTCG[C/G]TTATTT TCACTTGGTACGTCGTGAAGGACCGTTTCCAAATGAGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGCTGGGACACT
EST29912 3	103 C T	CTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATCTCTG T	ATTTATTAGTATCTGCTGTTGGGGTGGGGAGATTGTTTGAGATACTGCAACAGACACACAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[C/T]ACAGAGAATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTTACTGGCTTCACTGATGAGGCGAGTAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	---	---	AAATAATACATCATGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTTAAATATATCC[G/G]GATTTAAATTTCTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCACAATATAGGTAGC[G/A]ATAACCAGGCTCACCTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA AGAGTTTCAACATATAGGTAGCAGGATAACCAGGCTCACCTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AACAGGC	AAGAGAACAGGAAATATTGTGCTTTCTTG[G/A]GCCTGTTTCCCTATACCCCAATATCATAAGAAAT GTTGTTGCTTCTATAATGTTACGTTCAAAATCTTTTGCTTAATCAATCCAAATGAATTACCTGAATT TTCTCTCTTTGTTCAAAA

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCCAGCCCAACA/C/TGGAGGTGATTTGGTGGGAATCTTATCACAATTATCT
EST31968 8b	95 T G ...		---	CGAATTTGCTCTCTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAACGCCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTGCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAACGCCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTGCC
EST32063 2	103 C T ...		---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCTTCCAGACCTAGCTGGCTTGTAGT/C/TGTTCCAGGCCCATTTGAAATAGCAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G ...		---	AAGGCTTTCGAAGCATTCAAAGGCACCTTGGGTGTTGTGCTCTAAGTTCTGGTCACTGCAGCCCCJAG JTCTGTATTAGGGAGCACCCCCAAGCCAGTAACAATATGGTCTTGGCAG
WI-17800	29 C G	GGGAGCACAA GAGAAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAAACTCAGT/C/GAAGACTGGGATTAAATTTAGGAAATATTTACACAG TTTCCACAAGTCAGAAGAGCTAATCCCAACCCCTGTATCTGGAACATACACTGCTGCCATTTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCAATTCCTAAAGTCTGGGATGACTTTCCT/GJATTCATCAAGTAGAACCTAAGCCAAAT TCAGAAATCAGAAATCCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATGTTCATTTCT GTATCTGATGTAGTTAAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGAAACAAATCTTTA TAGTGTCCTAAAGATAATTAATTTCTGGTTTAAATCTTTGCCAGCAAAGCAAATAT/T/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAAATGTTT/A/TJTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAAACTACCA
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	GAAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGAG/AJACTGGATGCCAAAGAGTATGG
EST33301 4c	80 G A ...		---	GAAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT/G/AJ ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A ...		---	
EST33460 1	44 G A CA	AGCGTGGTTTT CAATACTAAA	CTGTATTATT GTTAAATATTT GCAITGTT	CTATCCAAAGATATTTATTGCAAGCGTGGTTTTCAATACTAAACA/GJATGTAAACAATGCAAAATATT TAACAATAAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACCTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACAC[AG]TACGGGAATTAC TATTAAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACACAAATGA
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA AT	AACTACTAGCG AGAACAACATA ATAAAATC	GTTTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAATGTGTGCCAAATACTCAAGTGTGAA T[AG]GATTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTCAGC TTACAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C]ATACAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTTAAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATATACTCCTAAAAGC[C]TGGGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAAGTTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTATGATAAAAACACCTCTCATTTGTGA AAAAACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATGT[AC]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84 A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCCGAGTGTGATGGTGAAGCAGCATGAAAACAACATCTCCCCAGGCCCTCGCAGT AGAGGCGAAGGGAACAG[AG]GCTGCCCATGTGCCTGTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G	---	---	ATTCTTTATAAAAACACCATGTCCCTAAAATGT[C]GATTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAAGGTGCTCTTCC[C]GTTTCTAACTCCCTGGACTCCCTCATTTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G	CACAGCCCTGC OCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTTACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCCC[AG]TCTTGA GATTCAGAAATCCAGAGGGTGTCTCAGTCTTGGTTTAGGTGCTTCTGTGACATTTTCCCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAATGCTACATAGGCTCCCTGAGTTCCTTTCATGTACGAATCT[CT]GGTTACACATCTT A/GIACAGCAGAGCTGCTGAGGGAGGGTGTGTTTAAATGCTGATGCTGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	CTGAGTTCCT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAATGCTACATAGGCTCCCTGAGTTCCTTTCATGTACGAATCT[CT]GGTTACACATCTT AGAACAGCAGAGCTGCTGAGGGAGGGTGTGTTTAAATGCTGATGCTGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGG GAGTAAA	CGTACCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA[AG]ATGGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGATTTTGCICAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	G A A G A	GTAGTGTGCTA AGTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAACCCGTGTGGGTAGCTGCTAAGCTGTATTTCAGA[G/A]GAATGTACAC AATCATACCACCTGGGAGAGAAAGAGTAAAGACACAGTCTTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T C A A	GCATAAAATT TTCAGTTGGT	CCCTCGGCACC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAATTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	A C I GTGTAT	AACCCACTAC TACTCAGAGT	AAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT[C/J]ATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	C T ---		---	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG TTTGACITTTAT[C/J]TCTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65	G A ---		---	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCC[G/ A]TGTGTGACITTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41	T C AGTCTCTC	GCAAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCTT[C/J]TGTAAATTAATACTACTATGC CGTGTGACITTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18086	63	G A ---		---	GTGGGATCCTATAAAAGCAGCCATGTGTGAACAAATGATATGCACAGAAAGCATCTCT[G/A] TGGCTTTGTACCGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGIGITTTGAA
WI-18115b	71	C T ---		---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18115a	70	C T TT	TTAGTGTACCT TTGGTATCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18136	78	A G ---		---	TTTTGAGAAGCAGCTCTGTAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAACTCTCTCTTA GGTAATTTGC[A/G]TAAGACAATAAAAGCATTTTAAAGTCCACTGCCGCCCTTAGAAACT
WI-18169	115	A G GAAGCTC	CCATCTTTCCG	GAGTTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTATCCAAAGCAGCCATCTTCCGGAAGCTC[A/G]TGGAGCACACAAGCAGA ACTCGGTGGGTAGATGGA
WI-18190b	26	G A ---		---	TGAAAGAAAGTCGACACAGCGGACACT[G/A]TCAATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAACTCTGGCGA

WI-18190	62 G A	TGAAAGAGTCGACACAGCGGACACTGTCTAAGTGGAAACAAGGATGAAGCTAATCATGTGA[G/A] GCAAGCTCCTCGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAAATCCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	...	GACAGTGAACAACATTGAAACACAAATACAACAACAAATAGGAACAAGAAATGTGTAATCCAA TGTTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTTCTTGAAC
WI-18215	78 G A	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT CCCC	...	ATTATACAAGCATTCTGAGTACAACTAGGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGGGGGAGAGAGGGGATTGAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A A	TGGTGTGATT GTGATACACTT A A	AAATAAAGGT TTTCAGGGGT C	...	CATTTCCGAAAACTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/G]AA CCCCTGAAAAACCTTTATTTTGAATTTGAAGTTTGTCTAGAACTGGGACAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	GGAAACTTG AGTTGAGATC A C A	CACAGAAGTG AATAGACTAGT GAGACA	...	TTTAAAAATGCTTAGATTTTCTCAGTATTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGGCATTTGGCAGAACTGGC
WI-18242	30 G A A	CCCCAAATGTT AATCGTAACA A A	GCTAACACTTC TACTGTAACAG CTTTC	...	AATATCCCAAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTACAGTAGAAGTGTAGCAAAAT TGGATGCCACAACTTATCTACCACTCTTCAAGCAAGTGAGGGTCAGAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAG
WI-18266c	119 C T	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAAGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAAGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC T T C A A A	TTTCATGCATCA TTTGTGCA	...	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAAGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	...	CTGAGCCCTCTGGATATGTGGTTTAGTGTCTATCATTAATTTTGGAAAGCTGCAGCTATTGTTATTC AAAT[A/G]ATCTCTGCTCCCTTTCTCCCTTTTCTGGGATTCTCATTCGATGTGTTATA
WI-18330b	66 A G	AAACATCTACAGCTGTCTTAGGCCATCCTGTGAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGGI A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAAATAAGAACATAATTTTGTGAT TCACA

WI-18330a	49 G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTGAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGTAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85 T C A G A	AAATTC AAGC CATCTACAAA	CTATGAGGCC TCAATGAGA	AAATTAGTAGCCATAACAGGCTGGAATTGCTGGTAGAATCTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT[C]CTCATTGAGGCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104 G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAGGGGATTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTCCCAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATCGGAGGCAGA GT
EST37624 6b	102 G A ---		---	GTGGCAAGCAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCGGTGCTTGGCTCTCTGGACG[G/A]TTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58 C T ---		---	GTGGCAAGCAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCAC[G]GCTGA TGGCCTGCAGTCTCTGCGGTGCTTGGCTCTCTGGACGTTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89 C G GCATCAA	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAGTCTTACCGTGTGAGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAA[C]GTCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117 A G ---		---	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGA[G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113 G A ---		---	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGA[G]GTGAAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112 C T CCCTT	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
WI-18012b	46 T C ---		---	
EST38390 4	75 A G CTCTGCATTG	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGT/AATCCCATGGTTATGTTACATGGCAAAAGGACTC TGCATTGT[A/G]ATTAAAGTTTATTATATCAGCTGACTTTAGCATTGGGAGATTATCTGGAT

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CAC TGCAC TCT GGGAAGC	TAATAAAAAC TGACCCAA TTTGGTAAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAA TACTTCGTTG/GCTCCAGAGTGCAGTGAATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACTCC TAAAAGATCT	TCTGTTAGGAC TTGGGGGA	CCTGCACTCC TAAAGATCTTTTTC/JTCCCCCAAGTCTTAACAGAATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGATTGCTGCTCTCGTTTCAGCTTTGATTTTTTGCTCTTGAGAACCTTG TCCTCCCTGCTGATT
EST38575 1		GAACATCCCA TGTTCTGTTT	AGGGAAGGTA GTATAACACAT	AGTGGTCAAAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTCTGTTTAAJ T/CJCTCTTATGTGTATACTACCTTCCCTTCTCTTCTTATACACATAGATTTTCCCTTAAATTGCAGC CCA
EST38616 9		CCTGCTCGGC CTTC	GAGGAATGGAT GGTGCC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCTCAGCCCGGGGGCCCGGTGG AGTCTCCGCGGGCCCGCCCTGCTCCGCCCTT[C/C/G]GCCACCATCCATTCCTCCAGGGG
EST38652 8		TCTGAAC TGGG CATTCAA	TTGCAAAAATG AAAGGAAAA	TATAGTAGGTACTTTCTTCTGCTGCAGCAGGAATTAATCAGTCTGAAC TGGGCAATTCAA[T/C]GCGTG GTATTTTTTCTTTCATTTTTCAGTAAGTAAAAAATCAT
EST38654 5		AATGGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAATGGTCAATTTAATATATCAGTTTTACATA[T/C]AGATAGAAGATTAAGGACCAT CACTGAGTCAATAGTCTCAGAGGACAGTTAAGATTTGGACCCAGGAGTTGGTTCCAGCATATA
EST38707 9			ATC	GGATCTCACTACCTGGGACAGCTGAGAAGGACATCCACCAAGAACCTACTGATCTGGAGTCCCA CGTTCCOC[J/G]AGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTCAGGAACACGAGG ATTCTTGCTTTCTGGAAA
EST38759 2		TGCTCCCTGA GGTGATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACCTACCTTTTGATGCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG[J/G]CCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC TAGCAGCACC
EST38775 1		AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATCAA	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGCT/JATTTGAATTCAGAGCAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAACCAACATGGTGG
EST38815 4		TGTTTATGAGA ACCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTGTTCAATCAACAAG TGTTTATGAGAACCCATTACACA[C/A]AAGCATGTGCCAGTCAAGCAGATTCTGTAATAA
EST38858 4		CACGAGTAAA AAGAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTGGGGTTTCCCATATTGTTATTGTTATTATTA TTCAACACGAGTAAAAGAAACTCATGAC[C/J]TCTCTTGAGCTCGCTCTCTCCCAATCTCGAT ACCGACTGCCTGTTG
EST38865 2		GCTGTAGAATT TGTTGATGC	GGAAGGACGG AGGACACAG	CCCTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGC[T/C]CTGTGCTCTCTCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTATGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCT CA	CCAAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAATTCJTGAGGACATGAGATT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGAAATTTGAAACATTTCCC TTATCAATGTCTACACATCTTTATTTTATTTTATTTTACCTTTCTCAAATATCGGATTGTTC TCATGAGAAATATGGCTGAGGGAGCTGGCAGGCTCTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TTATCAATGTCTACACATCTTCTTATTTATTTATTCJTTGTTTTTCACTTTCTCAAATATCGGATTGT TGCTCATGAGAAATATGGCTGAGGGAGCTGGCAGGCTCTCTCAGGCTCCTGAGCTCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCCTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATCAATGTCTACACATCTTCTTATTTATTTATTCJTTGTTTTTCACTTTCTCAAATATCGGATTGT TGCTCATGAGAAATATGGCTGAGGGAGCTGGCAGGCTCTCTCAGGCTCCTGAGCTCCTGGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAACG	GGTATTTGTG ATCCCATCTT T	GCACTAACTAACTTCAATTTGTGGATTGCACAGCATGGCTAAACCG[AG]TAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACCTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	AACCTGAATGGCAGTGAACACATACACATCAAACTTAGGGAATGTGGTTAGTGTGGTACGTTGAG GGAACTTATAACCTCAC[AG]CGCTTTTTCACAAAAACACAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	TGAATCCCTT GGTGG	CACTGCAATCT CAOCCC	TAAACATCCCATTTGAATCCCTTGGTGGG[G]CGGGGGGGGTGAGATTGCAGTCTCAAGATAAA TATCACAATATATCAAAACCTTCAAATTTCTATGCATTCACACACTGACATGAGCCACAAACATT CCTTTCACAGGACTGTAC
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG CTG	CCTGCTATGATGCCCTGGGAGATCCCGGACCTTCGGTGACQ[GA]CAGGCTCCCTGCCAGGGCTTGG CCCCGACCCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGTAAAG CCTAAGGAAT	ATCTCGGCTGG CGC	CACGTGGCCCCAAGTTCCGGGCTTCTCAGTCTGGATGGCTGTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGGAGGGGGGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTGT GAAAAATATA TTGATAT	AAAGATAATGTCAATCACAAGCAACATATAGAAACATAAAAGAAAAATAAAGTATCCACCCTAAAT CCCTATTATCCATGATATTTTCA[TC]JAGCAACTAGTATATATCAATATATTTTTCACAAACCCT TCAGTTACAC
WI-16403	69 T C	CCTTTGCCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTCATGTAATTTTCTCATTTTCTCTATCAGGTTTCTGGTCCCTTTGCTCAATTTTAACTT T/CCTTTTATATAGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCCCAAGTT
WI-16406	24 C T	GCITTAATGGC TACAGAAAGA AGG	CCAGAACCCAG ATGTGTTTAA AA	GCITTAATGGCTACAGAAAGAGC[CT]GGGTTTTATTTCTTTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCTCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGAAATAAACTTCCGTGCTAATTTCCAA[C/G]ACTATGTT TAATGTGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGOC	GCACAAATTA ACATAGTACCG AGAA	CAACAGACCTTGGTTTGGCTCACCTGGTGACAGGAGACTCTACCTGAACAGGGATGCC[G/T] TTCTGGTACTATGTTTAAATTGTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTACCCCAAGCC AGCTGCTGTCTGTCAT
EST39366 2	72 T C		...	AGAAACATTTCTGCTGATCAGAGGAAGATGTATGTAGAAAATCAGAAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGGAAGAAAATGTTTGATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGAGG TT	TGATTTGAGAC ATTTCACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTAAATCCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAATCAAATGCTTCTTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177	23 A G		...	ACAAGTGACATATCCAAACCAAC[A/G]TCCATCCCCACCTGTGCCCTATTCTTCCCTGTGTTCTTT AGAGCCTTTTCAGCTATTTCTGTGAAGCAAACTGCACGAAGGCTCCCCGTACTCTCCCCCTGGAA G
EST39428 8	31 C T	GCCTCCCA ATTGATT	GGTCCCTTATG AAGCCACC	AGTTCTCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCTATAAGGGACCCAGGATTCTGCATT TTCTGGTGGGCTAGGTAATTTCTGTGCTTTTGGTCCACAGAGCACAAATTAAGAAGATCAGGTCT GGCTGTTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT C	CAGGGGTGGG GATTG	AATTTAGCAGAAAACAATGAAGTTGGCAGAGGAATAAAGTATGTT[C/A/C]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA GAGTAA	TCCTGGAAAC TGACATAAAC	AAAGCCCTGTAACTGAAGCTAGACAACGTCAACTTTGGAAAGAAAATACAGGAACCTATTATAT ACGTAATCAGTTTATACCTGCCTACTGACATAGGACTTCAGAGTAAAT[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGC	CAATCTGGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATACATAAACGAACCTGAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCAGATTGGGTGTTTACAGGCGAGAGGGTGAAGACCAG
EST39501 0	81 A G	AAAGATTCT GTAGACATCT AACATTAG	CACCTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C		...	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGCTTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACACAGTGTGGTGTG
EST40601 9	78 A G	GCGTGGAACTT GAAACAC	TTCTTGGGAAGA AAGGGTC	GCTATGTAGACATAAAGA TCCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGGTGACTCGCGTGGA ACCTGAAACACACAGGACCCCTTCTCCAAAGAGGGCTGTGGCGATCAGGCCCACTCAAGG
EST41935	32 A G	AGTGATACAC ATCTTCAGGAT	GCACACCTTC ACACTGTTA	TCCATTGAGTATACATCTTCAGGATAGGTAGJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGG	AAAACCTGATTT GTTAAACATG	ATGTCATCTGGCTTTTATTTTGGACA[C/T]GTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA CCTTTGAACATCAAAAGAAATACAATATATTTTCAAAAATTTCTCATCACTGTAAATTCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC	AAATCTCAGC ATTGCTATAAG	AGAGACACAAGAAGAATAAGGAAAATGGGAAGAACAGAGTGAATTAAGCAAAATCTTGGG TTCAGATCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAT[C/G]CTTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG	CCAAGATTTCG TTTAATTTTAC	AGAGAGACAACAAGAAGATAAGGAAAATGGGAAGAA[C/T]AGAGTGAATTAAGCAAAATCTT GGATTGAGATTCATTAAACAGGAAGTTTCTCAAAAAAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCTGTGCT AGACAGATTTC	...	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCTGTG CTAGACAGATTCA[C/T]GCACACAACAACAGGAGGTGGGGTCAACGCGGAGAGGCCAAAGAC TAGGGC
WI-18425	81 A C	CTTTGGGCTCT AAGTGGGACT	OCTCCTGTGTG TGTTGCA	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCTGTG CTAGACAGATTCA[C/T]GCACACAACAACAGGAGGTGGGGTCAACGCGGAGAGGCCAAAGAC TAGGGC
WI-18449	129 C T	CTTTGGGCTCT AAGTGGGACT	CTCCTGACT GTATCCAGA	AAATTGAGTCCGGGTGGAACTATAAAAGGAAAGGAAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGATTGCTGATCTAAGCTGCTGTCCAGTTCCTTTTGGCTCTAAGTGGGACTA[C/T]TC TGGATACAGTCAGGGGAG
WI-18457	120 T C	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTCCCCCAAGACATTATTTTATCTT AAATGTCCAAATATCTGCTGATGCTGTGTTGTGTCACATTGGGGCCACAGT[C/J]AATAGGCTAAA AGGCAGTCCCACTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTCT	GGTGTATAGCTGCTGTACACCAATGGCAGAGGTGA[C/J]TAGAAACCATCTCAAGCCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGTCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60 C T	GCTGGGGTGC GAGG	GCACGATGGGA GTGAOC	TGAGGACGTGTGACAAGCTCAGCAGGGGTGGGGCGGGCTGAGGGTGGGGGTGCGAGG[C/T]GGT CACTCCATCGTGCCCTGGCCGCTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT

WI-18491	109	GA	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCTTGTAAATCC	CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAT GGTAGGTGGTATTAACTATTATTAAATCCAGAATGAC[G/A]GGATTACAAGAAAATGCACA CGT
EST50757 b	79	CT	GAGCTCGAGG CTGCTTCT	ACCTTCACCC GCCC	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCGAGAGCTCGAGGCTGCTTCTTTTATAT GTGCAGGGCC[C/T]GGGCGGGTGAAGGGTCAGAGA
WI-17675	103	TC	GGACATTTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAAGATCTTACCAGGTGCTGAAGAAAAGTGCTCTCGTTTAAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTGACTT[C/C]CCTGGTGGTCCCCATAGATTACCAT TGCTCTAATGGTGCTA
WI-16543	67	GT	AGATAAACTA CATTTGGGTT	GATTCATCAT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCTGAATGTCAAAACAAAGAGATAAACTACATTTGGGTTTGG G/TAAAGTCCCTGTATGATGAATCAAGATCCTCAAGTCTGTCTTGCCACCCATTAAATACGTATT TTTGTAAAGGCTGAAGTT
WI-17687	107	CG	GCCAAAAGG TTGGGAA	TTACTTTTGT CCGACCAAGCA	ATCTGAGATGGAAGAGTTTTCATCCCAAAACCATCTCCCCCTGACCCAGTCCATGGAATAATGTC TTCCACAAAACCGGTCCTGTGGTGGCAAAAGGTTGGGA[C/G]TGCTGGTGGTACAAAAGTAATT G
WI-17690b	79	AG	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG/G]ATTACAGGACCCATAACTCTTGTCTCACATCTGCTATGCTGCTG
WI-17690a	63	GA	AGGCATTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTT[G/A]A TTTGGCTTCCCTATAGATTACAGACCCATAACTCTTGTCTCACATCTGCTATGCTGCTG
EST51717 b	128	CT	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCCAGATTAT[C/T]TGAAGTGGAAACCCACCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAAGTGTTCGAG CTGGATTATTGCCTCAAA
EST51717 a	39	CT	GATCCAATCTCAGTGTCTAACTCATCCAGATTAT[C/T]TGAAGTGGAAACCCACCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAAGTGTTCGAG CTGGATTATTGCCTCAAA
EST53012	97	CT	TGGTCACTTTG GGGOC	GGCTCTGCOCA GGC	TTTCCAGGTTGACAGGTTTATCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGGAGAGGCGGCTGGGTTTACATCTCTGT GGGAGGTTGGGACAC
EST53349	96	AG	TGTTGAAAGC AGTCACAATG GTAC	CATCTGGATAT CTTGTACATTT TT	AAACTGCAAAATAACAAAACAAACAGAGTCCAAAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCAATGTAC[A/G]AAAATGTGACAAGATAATCCAGATGTTTAA
EST53389	74	AG	GGAGACCTGC AGAACTTAAA GCA	GCCCTTCTAA CAATAAATGCT C	TTTCAATGTCTCCTCCTGACTTGACAGACTGAGAGCCAGCCAGGAGGAGACCTGCAGAACT TAAACAC[AG/G]AGGACATTTATGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTAAACATGAAC ACATTAAGGGAGATGGCC

[illegible]

[illegible]

TIGR- A003P30	117 C G	---	---	ACAAGTTCAAAGGAGAACTTCCTTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCTCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA/C/GJACTGGCTGCCTGAA GGTACCCTTGGAGATACT
TIGR- A004S34	156 C T A	CCAAACCTCCT CATTCTATAA	TGTAACAGCT AACTGTTTTTG TTAAA	GCTTGCTTTTATGTTTAGTTCGGGGGAAGGAGGGCTGACAACCCGACACATCTGGACACCAGC AAGGTCACAGGGGAGTTTGCAAACTCTTTTGCTTGGCTAACAGTGTGTCATGTGACATAGCCA AACCTCCTCAATCCTATAAA/C/TJCTTAAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C	---	---	AACAACAGTGTAACTCTTTAACAGGGGATGTTAAAGGTAAAGTCAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTTGCATGGCGATT/CJAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA	GGAGATAAA CCAAATGAT	GCCATGCAAAA TTCITTATCA	AACAACAGTGTAACTCTTTAACAGGGGATGTTAAAGGTAAAGTCAGGAAGATAAACCAAAATGAT TGA/G/ATATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60 T C	CAGGAAACA GGCATTCTCT	TCCTCCACA AAAGGC	CCTACAATCCTATAATATTCGAAGGGTGGGAGGATGCAGGAAACAGGCATTCCTTAT/CJGCC TTTGTGGGAGGATCAATTTGGTGCATGCACCTTAGGGGACAATTTGGCAGTAGCTGTCAAATTC AGTAGCTCAAAATTTCAA
TIGR- A004V26	125 A G	---	---	TCTAGCTATAAGACCAGATTTTAAATATCTAGATATAGAATTATCCAGAATAATCTTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCAATTATCTTCACATGA/CJAAAGGT TTCAGTTTATAAATGCTTAAATAGTATCTATTTGCTTAAATAGTATCTATTTGG
TIGR- A004V28 a	29 A G	TGTTGGGGTG CGATCTC	CGGAGGTTGCA GTGAGC	CCAGGCTAATGTTGTGGTGGGATCTC/CJGCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCCTCTGCTCAGCCTCTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACTAATTTTG TATTTTGTAGTAGACATTGTATTTTGTAGTAGACAGG
TIGR- A004X20	25 T C GA	AAGTTTCCCT CTCTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTCCCTCTCTCTGTAGGA/CJGCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACTCTGGGCTCGCTTCAGAGGAGTTTGATATTTGGAAAGTGAGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTTCTTTCATTTCTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATGTCCCAATC ATCATCATGTCTCT
TIGR- A004X30	26 T C	TTTGAATCTT AGAGTAGAAC CCAC	TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAATCTTAGAGTAGAACCCAC/CJACTCTAGTAATACTTGTAAATAAAATAGTTTT AAACACTTCCATAAAGAAATTAGGGTGCCAGCTCTTGTATTTCCCTTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT	TTTCAATTTGGT TTCATTTGAGT	CTTATAATTAG AAATTTTCATGA AAGCAA	CACGGTATATGCCCTTATATAGGTATATATACAGATCGTACACATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCAATTTGGGTATGCAAAACT/CJTTGCTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTCTTTCATATTCATTTCAATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCCTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAAC T GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGGAGAGAACAACTGC AGCATTTTTTCTTTTTC/TCTTCCCGATGACCATCTTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTCTTATGTAGAGACTGAGGATCTGGTATAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCGG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAAGGGCCAGGTAGCCTTCAGGGGCGGGCA GGGTTGGGGAGGTAGGAGACTCTGGACCCGCGAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC/TCTGTAGATCTCTTGGCCTCTCTGTGAGGATTCCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAACTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC/TCTGTAGATCTCTTGGCCTCTCTGTGAGGATTCCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAA CTGTTACAC	TTGTCTATTAT TTAAGGCCAAC AAAA	CATCAGTAACATATACACAATTGGTCATCAACTGMACTTGGCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACTGTACACT/GTJTITTTGGCTTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAGAGTACTTTGTTAGACAAGTGAATCTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACCCAGGCCTCTG/ACTCAGAGCTGACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTGGCTGGCTTGGCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAAAAACTTTGTAGGGAAAAAATAAATCAATGGATATATGGGAAGAGAAAGTG CCAGGCTGGATGGTGTGAGACAGAAATGACCCCTTGGGCTCTTATTTTGTCTTTTCAACAGGAACC CCACAGATATTTGCGGTATGTCATGAGGACTGGGGATGCTTCTATTG/CJGGATGCTTCTATTTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTACTGCACCTTACAGAG/GTCAATTTCCCTGATTTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGAAGTATAAAATGTTGTATTTAAGAGAATCCCACAAG CTTGGTATAAGGCAGAAAATAAATGGTATAAGGCAGAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTCTAAGCACTTACTGCTATCAGGCACCTGACTCGG TGCTTTAC/GJACATTTACCTCAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGAGGAGAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGGCTTAGGGTGTCTCCCCACAGAGAGATACCTTGAACCG ACTCAATTCCTGTGTAAAGAGACACTTTGTCTGCTTACAGGACCTCCCCAAAGTGTGACAGATTCTAT ATAGGATGCTGGATTAGTTCTCTTGATATTGTAAAAATCCCCCAAGAGCCGCATATGAAATCTGCCC

X57830	106	G C	CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTG/CJATGCCATATTTATCTGTCAAT GAAAGCGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTACAGCTGTGAG CTTTC
X74070b	72	T G	TGGATC	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATC/TGJGATAAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTT CAGTTTGTCTTATACACAATTCATTCTTTCAGCTAATTAAGCCGAAGAGCCCTGGGAATCAAGTTT GAA
Z48804	44	C T	---	---	---	ACTGCCAAGTGTAGCGGCCCCCAACCCTTGCTCTCATCACCAAG/C/TJTAGAGCTTCTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACGTTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTGGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G	---	---	---	ATGACCAAGCCACCACATTTAGAACCTTGGCTGGCTTTGGAAAGTCCAGAGCTGGATCTCAGCTCC CGCCCCAGAGGGTCAAGCACCTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGCJAV GJTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	---	---	CCACTCCATCCTGATGCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAAJAGJTTCTCCAAGTATCCTACCTCCCTACTCCTGACACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCCTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G	---	---	---	CCACTCCATCCTGATGCCCAJAGJTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAAGTATCCTACCTCCCTACTCCTGACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCCTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A	---	---	---	CTCCCTGCCCTCCTCCTCCTGCTGCTGCTCCGCTCAAAACAGCCGAACCTGCTTGCATGGGGG GAGGGGGGTTTCTG/CJCTTCTCCTTCTTGGCTTCTTATTCTCCACAAACCAATTCCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCAGGGCCACCTCCTGCTCCTCACTGCTGCTGCTGCTGCTGCTTTT CTGGA
D37931	64	T C	---	---	---	ATTATCGCAGTGTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/T/CJ CCCAGGCTCTGCTCCTCAGCTCATTTCTACTCTTTTCTCTATAAAGTCAATTTTAAATACATTT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101 C T	---			CAGCAGGACCTTCAGTGTGATCCCTGCGCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTAGAGGGAGTGATTTTCCCTGTTCCAC/C/JGAGAGGAGACTTTTGTTCACAAATGGATCAC AATGAGAGGAGTCTGTTCTCTCCCGCTCGCTCTCGGTGCTGGAGGGTGACCTGTCCAGATGAC
D90145	21 T C	---			TGGAAACATGCGTGTGACCTC/C/JACAGCTACCTCTCTATGAGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTCTTAACCTAAATTTAAATTTATATACATACTATTAGTTTTTATAATTTATTTTGAT TTACAGAGTGTGTTGTGATGTTGCTCTGAGAGTTCCCGCTGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035	59 T C	---			ATTATCACTCTCAAAAATTTGGTGTGTGTGTTAAGTACTTCTTATTTATGAGCCCC/C/JGAGGA CCAGACATGTTATTATCAAGCCCCCTTATATACCATCTAAAT
EST16668	71 C T	---			GCATTTTAAAAATTCACATTGAATCATTATTACTATTATGATGTTTACATAACAATTCAGTATCAAT ATG/C/JTGTAGATTTCAGATGTAGGTCGTCATACTGAGCAGCTTATCT
EST16904	57 C T	---			ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAATAAATTACA/C/JGAGATA TTCACACTTTATTATAAATAGGGTTTGTGTAGATGATTTTCCCAACTGTAGGTTAAACAT
EST21863	49 A G	---			TTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACGTATACACC/C/JGTTACTACTTACTC TTCACCTCTCAAACTGATTCCTCTAAAGACTTCTACTTAGCAA
EST21885	80 G A	---			GGCTGTAAGTAGAATCAAGTTAAGAACATTTTATGCCTTATCCACAACATTTTACTGAGCATA CTAGGTGCTGGG/C/JTGTGACAGTGAGCAAAAACACAA
EST22623	26 A G	---			ATTTTAGTGAATGACAAAGCCCCAA/C/JGAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22644	98 A G	---			AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/C/JGAAATGTGGAAGATGGCTTTTAAACCC
EST23587	31 T A	---			CCTCATTTATTTAAAAAGACGGACATAAAAA/C/JATACAAACAAAAAACCCCAAGTCACATTTTCAG GAGGTAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246	106 T C	---			AAAGATCTGGCATTATTCACATCACTTCTAAATATTTTGTAAATACITTTTCCATGAGTATTTTTCA TGTCGAAGCATTTTAACTATCAITTTAGCGTAAATACC/C/JGAATAACCCCATAGTTACAGAATTGG GTCTGTGAACCTCAAT
EST24308	45 A G	---			TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/C/JGATTTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435	73 G A	---			CTTGAACCTTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/C/JATJGCCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTGTTTC
EST25089	25 T C	---			TATTGTTGCATTATCAAAATGGTT/C/JAGTTTTCAATTAACACTGTAATGATTCTATGTATAAA ACAGCTTGAAGTTGTAATGTAGTTTCCAAATCGTTAGTTAATGCTACAT

EST25476 9	33 GA ---				AATGATCTTTATTTTCAGACCTGCTCCTAAA[G/A]CTTTCTCCTCCTCTAAACCAACACA AGAGGTCCTCTTGCTGCCCTTCCATGGACTGTGGCGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---				AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACCTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATTTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---				AGAAAATAAGGTGCTACAGAACTCATGT[C]GATAGCGCTTCTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTATATCACACACACTGTGCCCTAACACAAACACGGTGACTCTGA
EST27816 5a	26 T C ---				CAACTCAAGGTACAAGACAATTGCATT[C]TAACATTGTTATAATAAAGGAACATCAGATCAAT CATTAAGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 A T ---				GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGAT
EST30226 5	25 A C ---				TACTCACCCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAACTTCTATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 C G ---				AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTGTGAGG
EST32515 7	25 GA ---				CCGAATATAAGGAAAAAATGGTGG[C/G]ATGCCCTTAAACCTGTTGAATAGATAATATGGCCAAAT ATTACAGTTTCTCACCTTCTCTATGAATACTGGCAGCTGTTATTTTCATGTTATGTGAGTTTCTATGC ATAAAAATCCCAAGTAAGA
EST33274 4	27 T C ---				TGCTTTGTTTCCCTCCAAATCCTAAAAT[C]GTGTGCTTCAAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGTAACCATATTCAAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATT GGACTAGGTA
EST33352 7b	75 C G ---				TACACATTATTCAAGAGACCACCTGACATGCATCTCCTCCGCAAGATACATTCTCCTCTCTTAGAGA AGTTTAA[C/G]GACACATAGTATTATTTTACTAAGAGAATACTCTTGGTGTCATATCTAGGGG
EST33424 1	126 A C ---				ATTTTCCACAGCAGAAGTATATTATTGTGCTGAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACAGTACAGAATGTTTCAAAAAGATTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTGAATCCCTCT
EST33488 7	90 A G ---				CCTTGGGGGAGTTTAAAGCCAGAATGTGACAAAGTCACCTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCTCCAGTTAGGTTCTAGGCATATAAGCT GCTC
EST33508 1b	45 C T ---				AAAAACATGCTATTGAAACAACTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---			AAAACATGCTATTTGAACAAACCTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAAGCAGTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCCAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTTATCTTGGTTTTGAAAAATTATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAC[C/T]TCTTTGAACACTACAGCCTGAATCCCC
EST34739 3	97 T A ---			GAAGTATCCTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTC[T/A]GGTGCCTTACAACCTCCAACACTGCAGAAATTTCT TGTTGTCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCAGACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GATTCAGGAATTCCTAGTCCTATTACA AAGATTTGTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGTGCTTCTGGT[G/G]GGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TGTCTTCTGGTGGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---			CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			TCTTTTCAAAATTTTGTATGATGAGCATTTAATG[C/T]TATAAATTTCCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTTTCCATTTTAC[TAGTTCAGAACTTTTTCATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACITTTAGGCAATGGAA[C/T]JAGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTCCCTCTCTGAGGTGGCACCTTCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAAAGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATATTAACCTGAGGGAAACAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCTCCCATGAAACCAAGA[C/A]CTTGCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCTGTGA
EST36301 4	93 C T ---			CACCTGTTTCATTTGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCAAGCTACAGC AGTCAGGAGGAGCCCATGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCCACAAGACATGACTACCAACGG[G/T]GGCCCCCTGCACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCAIATACTGGCTGGCCTCTTCTCTGT CACAGGGTCTTAGTCGT

EST36620 6	50 GA ---	---	GACTTATTAGATAAGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 CG ---	---	CCTGTGATGTGCATGGGTGCTGAGCAGTCGTACTTACTATGCTGAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGATTCTTA[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 CT ---	---	GAGACAGAAGCCATCAGTTAAATGAGGTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACITTAGCTACCTGGACATGCTATCAAGTGTCTGGGAAGGGAG
EST36823 6	103 AT ---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 CG ---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTAAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGTATGCAGTTT[C/G]TTA GGGAATTAAGACAATGCAG
EST37054 3	88 TC ---	---	GGTCTACTCTCTGCCCCAGGAGGTTTGAACCTCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCTTAAAGTAACCACTGAA C
EST37269 3b	105 TG ---	---	AATAGTCTATGGCTACGGGCGGCGGATGTTAAAAATGGGATTTTAAATTAGATTGTGAACATG CAACCCAGCAAAATTTCTAGCTTATATTTGAAAGT[C/T]GICAGGAGAAAAATGGGGTCC
EST37284 2	93 GT ---	---	AAAAGACCTTTCTCAAGCAGTAACCTTTGAGCAGAGACTCAGATGAAGTAAGGATGAACCCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 AG ---	---	AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACATAAGATATCCTCCTGCTCAGCCTCCAGGTAGT TGGAACTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 CT ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCCAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 GC ---	---	GTGACATCATGTCTCTCAATGCCCTTCAATTAAATAGTAGTTGAGCGCTGGGGGCTGAAGTCAGACT CTCTGGGTTCAATCACAGTGTGTGCTCTGCA[G/C]GCTGTCTCCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41 TC ---	---	GTGACATCATGTCTCTCAATGCCCTTCAATTAAATAGTAGT[T/C]TGAAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAATCACAGTGTGTGCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G ---	---	ACACACAAAAAATGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCTGTGAAAAACIT/G JAACATGCCTCAAAAAAGAGGGGAAAAAACITTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---	---	AAGACATAAATCTGCAATGAATCAGTTATGAATAATTAAACCTCTG/AJCTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34 A G ---	---	CTAGGCATGGGGCTTTTACAGTCATTTATTTACC/A/GJGTCATGAATTCATTAAAAACCCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAATACCCCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTATACATGTTTATATCACTTAT/GJTTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGICTTATAGGGAAGACICTGAGGTTTCAGAA
EST38068 6	57 C T ---	---	TCTACAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTAC/TJCGCATGG AAGAAGCTCTCCTTTTAAITCCCTAACCTCTCTCTCTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---	---	TAAATCAAGGCCTCTTTTCATTACCAAAACAAAAACAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCGAAGTGTATCCTGACTGACIT/GJGTCCTGACGTGCCATGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C ---	---	TTATTGCAAAAGTAAGCAGCGGT/GJGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGAAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---	---	TTTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGTTTAAATATATCATTTTTATTGGGATGAGATCA TAGCTTTTACACAAATGCTATG/TJAAACAAAGTTACTGAATATTTTACCCTCGTGGAGTTG
EST39331 1	70 G C ---	---	TCCTTCTTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAAGACCAGCCATGGAAGGAAAGTA TGCG/GJGTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---	---	GTCACCATGACCTTACATAGTGCCTCTAGT/GJACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---	---	TTCTAATAGCATGCCCTGTGACAGGGGAAACTAAGCTC/TJCTCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTCTCCAGAAAGGCTCAAGGTGTC AATAATCTGTGGGACTCA
EST40549 1	42 A G ---	---	TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA/GJATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTGTACCACCATTTCTCACTTTGAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACITTTGGGGAG
EST40579 1	81 A C ---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTCACTCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA/AJGAGACTTGGAGACAGCGATTAAATACGGAACAAGGTTCTCCAGGAAG
EST40584 3	68 A G ---	---	TTGTATGGTTGTAGGAATTTGGGAAGAAATTATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A/A/GJTGCTGTACTCCCAATATCCTATGTTTAAAGCT

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EST51340	51 G A ---	---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	---	CATGGGAGTATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCTCTCTACAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCCTTTATCCAACTCTCGA T/CJTTCCTTGGTCTCCAGTGGAAAGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGAGT AGCTG
K01506	63 T C ---	---	---	CTGAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTCTCTCACTTCATGTGAAACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCAATCCT TAGTAAAGTTTCCAACAATAAGAAATTAATGACACTTTGGTAGCACAATAATGGAGATTATCCTTTC ATTGAGCCCTTTATCCT
L18877	69 T C ---	---	---	TGAGCTGAGCAGGATTGCAGCCAGGGCCAGTGGGAGGGAGTCTGGCCAGTGCACCTTCCAAGGCC C[T/C]ATCCATTAGTTCCACTGCTCGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGGTTCTGTCTATTGGATGACTTTGAGATTATCTTTGTTCCCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	---	GCTATTTTACATATCCAAAGCCCTTTAGGGCTACAGT[C/T]CTCTTGCTCGACCCCTGTAGGGTGCCA TTTGGAGTTACAGCCTAGAAAGAAAGGCTTTGGGCTGGTGGTGGCATAGGCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCGAGGAAGATAGCTTGAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	---	GGGTCCAGAAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACCAGCGTCCCGAC CC[G/C]CGTGGTGTAGTATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	---	ACTTGAGAAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTATTTCTTTGTATTTTGTATAT[T/G]CGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGTGGGCTGTGTTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	---	CAAAGTTGTCTCCTGCCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACCACCACAAATCTGAAC[G/A]JGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	---	AAGTGAACAGAGCAAGATGGATTGTTCCCTATAAAGCACATAGTATGTTTACTGGTATCGT AAGAAGCTGGAAGAGAGCTCAAGTTTGGTTTACITTCAGAAATC/GAAGAAGCTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAGTATCCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	---	GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACAGAACTG/AJTTTATTTACCC CCATCAAGTATAAGGTTACTGATTGATTGGTCCCTTTTATAACATTGGTATATTCCATTCATGCCAA AGCAAAAGAAGTAAAGCTAA
M19169	113 T C ---	---	---	TAGGATCTGTGCCAGGCCATTGCGACCCAGCCACCCACTCCACCCCTGTAGTCTCCACCC TGGACTGGTGGCCCCACCCCTGGGGAGGCCCTCCCATGTGCTG/C/GCCAAAGACAGACAGAG AAGCTGCAGGAGTCCCTTTGTTGCTCAGCAGGGGGCTCGGCCCTCCCTCTCTCTCTCTAATA GC
M21539	114 T G ---	---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCCTTAGCCCTGTGATCTGCCCATGATGATCCCGACAGCAAAAT/GJTTTCTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCTTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G ---	---	---	CCTAGCATTTTCTGGCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCCTCACCCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTCTTCTCAAGTGTACCTACTAAAG/GATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	---	CCTAGCATTTTCTGGCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCCTCACCCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTCTTCTCA/GJGTGTTACTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	---	CCTAGCATTTTCTGGCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCCTCACC TCTCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGAC TTCCTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	---	TAAGGCAGCTGTACGGAGGCCAGTACAGTCCAGCAATTCACAAACCCTTGAC/GCJAATGCT TGCCAAAGCTGTTTAAAGCCAAAGAACACCCCTTCTTTGTTCCAAATTAACCTTTAGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34 G A ---	---	---	ACTTACTACCTCACCTGCAGGCTGACGGGA/GAAGAACCACTGCACCACCGAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGCTTGTCTGGGAAGGGCCCTTGTCTGTCAAGGTTG CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCTCCCAAAAGGAGCTTGACTTGCAATTTCTACC T

U06641d	166	CT	---	CTCCTCCTTTATTTCAGCATGGAGGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAACATCTTTC ACAACTTACCTTGTTAAGACAATTTAAAAAGATCTTTTACAACTTACCTTGTTAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAATTTATCTATGTCAATGATTTTAAAGCTA TGAAATACAATGGGGGA
U09607	39	TC	---	GAGGCTTATGAGGGTCTCTACTTCAGGAACACCCCA[C/G]ACATTTGCATTTGGGGGGCTCCCG TGCCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTGGCCCAAGGAAGCAAGGAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	TC	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCTCATCTGGAGCCTC GGGAAGTCTGGTC[C/T]ACATCTGCCGCCCTTCCAGCCCTTCCCGAGCCCTCCTCTTGTCTTC ATTCAATCAACAAAATTTGGC
U10694	20	CG	---	GTGACATGAGGCCCCATTCTTC[G/G]CTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTGCGGTCTCTGTCTATGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATTTGTTCAATGTTCTTTTAAATGGTCAGTTTAAATGAACCTTCCACATCGAAGTTAA TGAATGACAGTA
U13877b	162	TC	---	AAAAGGACTCTGGTTCAATCCAGGTTCCATTTGCTATCTTTGTACCTTGCACAAAGTTGTTTAAAC CTCTTTGTTCCAGAAATTTCTCCATGGAGTAACAATATCTAGGTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCAAAGAGAT[C/T]TACCCTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187	TC	---	TTTCTGTCCACTTTCACCTGGTTTTTAATAGCCAGCCAGTCATATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C/T]TGGTCTCATAC CTCATATGCAGGATTCAITCA
U17077	122	TC	---	TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAAAGTCCACGGGATTACAGAAACGTCCTTGACAGCTAGCGATGACACACACAT[C/T]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCCCTGGGAAAACAACTGTCTCTTGG AATTA
U18543	58	TC	---	GCACATGCAGAAATAGACTCAGCCTATGTCTCTGATTCAGCTGGGTAGTCTAGAACTTT[C/J]AGAAG CTCCATCTTTTAAATGTTTTTATTTGTTATGTCCCCCTCCCGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACAGATGGTGTAGCTGAAGTTTGTAGCAATTAGGCACCTTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164	C A ---	---	TCACGTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTGTATATGAAAAATTATT ACTCTTTTGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGAC[A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C G ---	---	TCACGTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTGTATATGAAAAATTATT ACTCTTTTGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGCAATGACTATTCTCTG AAGACAAC[C]G[A]AGAGAAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A G ---	---	CAGGAGAGGTTATTCAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A]GJTT TTGAGTGACTGTGCCTGGTTGATTTTAAAGTAGTTCCTATTTCTATCCGCTTAAAGAAAAATT GCATGAACCTAGGCTTCTGTAATCAATATCCCAACATCTGCAATGGCAGCATTCGCCACCAACAAAA TCC
U28413	29	C T ---	---	ATTCTGCACAGCTAAATTAGCCCTAAATG[C]TJGGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCCCTTGATCC CAGATGTTGTGGCCTGGGAAGCCCTCATTGCTACAGTACAAGTAACACAAAGTCGTTGTACCTCAGTT G
U30884c	89	A G ---	---	TAGGGGTAGCATTAAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATCCCACGTTAGCCA[A]GJTTGTTCTTGATGAATCTATATAGTCAAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATACTGATGGCTTGAACCTGCCCCACAGTTGAACACAAGT GCTGTCA
U30884a	34	A G ---	---	TAGGGGTAGCATTAAAGATTCAGGAGTCATTAGC[A]GJTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCCACGTTAGCCAATTGTTCTTGATGAATCTATATAGTCAAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATACTGATGGCTTGAACCTGCCCCACAGTTGAACACAAGT GCTGTCA
U31216b	78	A G ---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTCA[CA]A[A]GJCCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCAGCCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A ---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC[G]A[ITCATCAAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCAGCCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ...				AGTTGCCAGCTCCCATGTACAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTTGGTTACAAATGCTAGGTCCTCCACTGCCTGCT GGAAGAAACACACACTCCCTTTGCTTAGCCCCACAGTTCTCCATTTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ...				AGTTGCCAGCTCCCATGTACAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCCCTACGCCACAAATCTGGTGCCTCTCTTGGTTACAAATGCTAGGTCCTCCACTGCCTGCTG GAAAGAAACACACACTCCCTTTGCTTAGCCCCACAGTTCTCCATTTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ...				ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCTCC AGACCGCAGG[C/T]TCCCCCAGCCTCAGGTTGCTGGAGCTGTACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTGCCTCTATCTGCGGGGACGCTGCTCGAGAGAGGCCGAGAGGCCGAGAAC ATGCCAGGTGTCC
U37690	54 A G ...				GACCACGCTGAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[G/C]CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCCTGGCCGAGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ...				TGAACCGTTTCAACATGGAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCTCTATACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ...				TCAAGAAGGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGGTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCCTGTTGGTTTAAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCTAGAAATTTGGATTCTCTGTTTTTTCATGCTCTCCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ...				AGGAAGATCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCCGAAAAGTTGCTGAAGGGAAGGAGACACATTACAAAGAAAGTTGGGAAAATTGCG AAATCTGTTGTGCA[C/T]GCTCAAATGAAACGCCCTTCGGCTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A/C ...				AGGAAGATCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCCGAAAAGTTGCTGAAGGGAAGGAGACACATTACAAAGAA[A/C]GTTGCGAAAATT GCGAAATCTGTTGTGCACGCTCAAATGAAACGCCCTTCGGCTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGCTTCTCTCCAC/GJTGACAGCTTCTGAGTACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCCAGGGCTCCAGGACTGGGGCTTGCCAGGCTTGTCAAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGTGGCAGGGCTGGCCCTTGTCGCCAGCCACCTGGCCCTTCTCC
X54869	99 A G ---	---	AAGCATTGGCGTTTACAGTGCATCAGATACATTTATATTTCTTAAATAGAAATATTATGATGCAT AAATCTGAAATGAATATGTTATTTGCTCT/GJATACAAAAATCTAAATCAATATTATGAAATAG GATGCACACAATTACTAAAGTACAGACATCTAGCAATTTGTGCGGCTCATTTTGTCAACATGGTA
X66924	147 G A ---	---	GCCGTGCTGACACCTCCAGAACGAGTGTGGGCGGCTTCTGGTGGGACCCCGGGAACCTCTC CTGCCGAAGCGGAGCGGAGGATGGGCCCCAACTTCGCCCTGCCACTTGACTTACGCAATCCCT TCCTGGAGACT/GJAACTTGGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA
X78932	62 T G ---	---	GAAATGTGAAGAAATGTGACAAAGCCCTTAAAGCGGTTGTACACACTTGTATATAGATAA/TGJT CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAACATTTAATTAATTCATACCTTA TTGCACAGGAAAGCATTTATCTAGAGAAAAATGTATAAGAAATGGAAGTGCATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25 T C ---	---	CTAACCCATAACTCAACACATCT/CJTATCTCCACCCACATCCACACACATCCACCTCCATCC CCAACCCATCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAGCCAGGGCCATCCCCAAACCCATCCCCAAGCC AACTCAACACCATCC
X80197b	99 G C ---	---	ACCCAACTCAAGTCCAGGCCCCAGGCATCTTCTGCCCTGCCTTGTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGCTCAGCTACTTCTCTCTG/CJACATTTGAAAGACCCCTCCACTCTGGCCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG
X80197a	28 A G ---	---	ACCCAACTCAAGTCCAGGCCCCAGGC/GJCTTCTCTGCCCTGCCTTGTGGCCCATCCAGTCC AGGCGCTGGAGCAAGTGCTCAGCTACTTCTCTGCACTTTGAAAGACCCCTCCACTCTGGCCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG
X85106	150 G A ---	---	GGCACCCAGAGTGACCAAGTCCAGAGGGAGCGCGCCGCTCGCCGTGTCCGTGTTTTCTTTTT CAGCCCGGAGAGTGCTGACCTGGGGCTTCTCCAGGCTCACTGGCCACGCTCCCGCCGCTCT CTTTTCTCCCAAGC/GJAAACCAATGCGCCCTTCACTCGCGTCCCGTGGAGCGCGGGGCTT CTTTCAGAGC
X87160	128 T G ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGGCCCGACAGCGTGTGCACAGGGGACCCCTCTGCCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCCTGCTTTAAACCGCAAGATGGGGCTT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACCTGTCCAGGCTGAGATAAATCCC GGGA

1282	130	C T ---	---	GTGCGATCACCACACAGTCTAAATTCAGATGTTTTCATACCCCTAAAAGAAATCTTGACCCATTAGCAATTTCTCTCATTCCCTGCCCCACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGCC[C/T]ACTTGACATATACATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACCTGAGAATAATGTTTTCAAGGT
6810	68	C T ---	---	AGTATCACACATCTTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAAAACTTTA/C/TJAGAAGCATTTTTTAATTTACAACACAAGCTCAACGAACCTACAATAAGTCTAGTAGTCTGTTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAAACCTTTAAAAATGCTCTATGAACAAGTACAAATTTCTTTTTGAGTTCTGCAGAGCAATGACCACIAAGAAATATTTTTAAAGGC
6817	118	A C ---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTATCCAGTTAAGACCAATCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCGAGGTAA/C/TJGTGGATACCCCTGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAGATGTGGACACCTTGTGTCAAATCTTTGGTTCAGGTGCGGCCCTGTGCAGATCGGCTTTTGGTTGGTGTCTTAG
6819b	212	C ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTGCATATACAAAAATTTCTGCTATTTTGTCTTAGCAAAAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCA
6819a	166	G T ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTTGTGCATATACAAAAATTTCTGCTATTTTGTCTTAGCAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCA
681xx	39	A G ---	---	CTGGTATGTCATAAGCAATCCATAATGTTTATAGCTATTTA/GTTTACTATGCGACCATTTGGGACACAGATTATATGTCAGACACCCAGCAATGTCTTAAAGATATGCAAGCAAGCACAAATCTGTCATGGTTAACAAAAAGAAATGAACGTCTAGG
6972b	149	G T ---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTTGGTAACTATTGATTATTGCCACAAATTCAGAGG/TCCCTGTTATTGGTCTATTGAGATTCACACTCTTCCCTGGTTAGTCTTGGGAGAGTGAIGTGTGAGGAAT
6972a	122	A G ---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTTGGTAA/GTCTATTGATTAATGCCACAAATTCAGAGCCTGTTATTGGTCTATTGAGATTCACACTCTTCCCTGGTTAGTCTTGGGAGAGTGAIGTGTGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTTCCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTTCCCT CAATGC[A/T]GA
7598i	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAG[C/T]GCTAACCCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA/GJAGGAAC TCAATGAATAAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACA/CJG]CCAAAGCCAAAGGAAC TCAATGAATAAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAATAAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTCTGCAGGCCGGAGCTGTCTCTATTCAGACATCTTGCCAGCTCTCTGTGA ATACTTTAAATGAATGGGTAGTCTATCTCTCAAGGTCCTCCCAAAATAT/TCCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTCTGCAGGCCGGAGCTGTCTCTATTCAGACATCTTGCCAGCTCTCTGTGA ATACTTTAAATGAATGGGTAGTCTATCTCTCAAGGTCCTCCCAAAATACCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTCTGCAGGCCGGAGCTGTCTCTATTCAGACATCTTGCCAGCTCTCTGTGA ATACTTTAAATGAATGGGTAGTCTATCTCTCAAGGTCCTCCCAAAATACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAATTTTATTAGAAAAGTGTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCCAGGTGG AAAATGGGTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCC/JG]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCAATTTGTTAATCACTGAATC TGGGTTTTCCTCTGAATTCACACAGAGCATGCACATACACACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA/CJTG]GTCATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACIG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG/JG]CGCAAAATCCACTTTGCTGTAAACGGTCAATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8498	84 C T ---	---	AGGTTTCAGGGTTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG/CJ]AATACCTTCATTAAATCGAAAAGAAAAATTGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCTCTCTCTCAATACAGAACCGAATGTAATTTTCTCACTCAG

WI-18562	29 G A ---	---	CTAAGGAAAAATTTAATGATGGAATATC[G/A]JACAATATTCAACATCATTTAAAAACAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51 A C ---	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]JGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGATAATTGTAAACCACAGTGTCTCGCACAGTTC AC
WI-18683	22 C T ---	---	TAAGCTGTTCAAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
WI-18520	75 G A ---	---	GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACCTACTACTGCCAACAAACACGGGATCCACTCTGCTTCAA TGCTCTTCCGTGAGAC
WI-18563	94 A G ---	---	AAATAAAGTTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 T A ---	---	GTCTATTTCAATTTAGCTAGACCCATTTCATCTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATCAGTGCCTAATTGAAGACATTTGGATCGTTTCCCAG
WI-18723f	94 G A ---	---	AACTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71 T C ---	---	AACTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT/CJACAGGTACATAGGTAACCAAAGTATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96 A G ---	---	AACTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18619	44 G A ---	---	TTTATTACAATATTAGGTGGCACAATAACTAACAAAGCTTCTGA[G/A]JACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAAACTCGAAATA
WI-18715	76 G A ---	---	TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAAGGGAGCCTCCAGGTGGAAAGGTTATTTTAAATAAAAAATAA TGGAGCTACAACCCACCCCC
WI-18535	107 G A ---	---	GTAAATAAGTTTTATTGGCACAGCCACGCTCGTTTCATTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGAGCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGTGTCOOOOGTG
D17525	107 C T ---	---	AGAGTGGTCAGAACACAGCCCGAATCCAGGCTCTATCACTTACTAGTTTTTTCAGTTCTGGGCAGGTGAC TTGATCTCTTCGAACCTTCAGTTTCTTCATAAGATGGAA[G/C]TGCATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAATGCACCTTAGCAGAAGGTGATGTTGTCTACCAGGCAGACGAAG

DWU-133c	313	A G	---			TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTGAATTTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C	---			TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTGAATTTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T	---			TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTGAATTTTAATAGTAACCTCC ITCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T	---			ATGAGATCCTTTAAATCCTTCATGAACGTTTTGTGGTGGCACCTCCTACGTCACAAACATGAAGTG TGTTTCTTCAGTGCACTGGGAAGATTTCTACCCTGACCAACAGTTCTCAGCTCCATTCGCCC CCTCATTTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGCTTTCTGAGGAG AAACAAATAGACCATAAAGGGAAAGGATTCATGTGGAATATAAGAT
DWU-387	169	G T	---			GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCAGTCCCAACAGTTCACTTCATATATAAAGCATTATTTTA CTCTTTTGAGGTGAATATAATTTATATTACAATGCTG/TAAGGCTTCTTTAATACTAAGTATTTTCA GGTCTTCAACCAAGTATCAAAAGTATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	---	---			ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAAGCTGCCAGTCAGAT GGGCTGTGCCATTTAAATCACTGTAATTAATAGTTTGAATAGACACAAAGCTTAGCTAATCAA CCATTATTTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTGTAG GCCCTTCTTCTTACAATGAAGAGATGATTTCTTAGTTATGGTTA
DWU-447	85	A G	---			ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAAGCTGCCAGTCAGAT GGGCTGTGCCATTTAAAGTACTGTAATTAATAGTTTGAATAGACACAAAGCTTAGCTAAT CAACCATATTTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTG TTAGGCCCTTCTTCTTACAATGAAGAGATGATTTCTTAGTTATGGTTA
DWU-476	63	C G	---			GTAAAAATTCAGTTTTTCCAGTTCCCTCTTTGTGCTGCTCTCAATTAGCGTTTAAAGGTGAGTCGAT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAAATCTATCACCATACAAAAATTA[A/T]TGCAGTATTTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	---	AAATCCAGGCATTTCGAATCTGTTTTTCATGATTTATAGAGGGTTACACAAAGTGCCACTTATTA AGAGCTTCACAGTGAAGATGGAGAAAGTGAACCTGCTTTGAATATCCAGATGTGTTGGTCA/G TGCGTATGGCAGTGAGCAGGTATGTGTTTGTCTTTGCTTGCTGCACTGAAAAATTAATGCTATCAAGAGC AACTATGAACGGTTTTTTTATCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAATTATCCAGGATGTGGCTCAITCTTTTCAGCTTGTCTTCTATACTGTTGTA ATATACAGTTTTGTAAACCATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATAATCTTGTCTTTCACAAATATAGTTGAACAAGATTCCCTAAAAAT CCACCAGGATTATCTCTAAATCTAGTCTGATTG
DWU-59	94 C T ---	---	---	CATTCTTTGTGAAGGTAATGGACTCACAAGGGGAAGAAACATGCTGAGAATGGAAGTCTACCCGG CCCTTCTTTGTGAACGTCACATTTGGC/CJGAGCCGTGTTTCCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGTGGGAATTTTGTTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCTTCGCTGCATTGCAGAGGAGAGCCAGGTCCTCCTGGAGAA/CJTG CTGCGTTCCCGAGCCCAACCCGGCTTGCACCACAGAGCTGTGAGGCAGGAGGTGGGTAAAGACGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGGACCTGCGGAGAGGAGCAGTCTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA/JGJGAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCAGAGTGGAAAAATTTTAAATCTTTTATAA/JA/JCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT/JCAAACCTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTATATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAAGCTTCCCTAAAGTGTCAAACTTTCATTACTGAGATTATTCAGGCCAAT GTGTC/JTGTGGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTTCTCTGTTTCA

WI-18063	105	G A ---	---	---	AGGCTTTAAACTGATAACAAATTTGCCCTTTAATCACATACAAAAAAGCTCGACATTTTCATCCCTTCCTTCG CCATGTTTCTGATTTGATGTAACATTTAAATTTGTGATCTTTAACAATATACGTAGCTGCA
WI-18078	86	A T ---	---	---	AGTTGAAAGATCAGAGAGGTTATGTTGGTAGTAGCTGAACCTCAGATCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAGATGTGTCCTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C ---	---	---	CCTAAGCTCACTCAGTATTTAATCATCTGCTAAATTTTCATCTTTGTTAATCCATCAGACACTGTGGT TTTCATCTCTAGAAAGTTTGACTTTCJGGGCCCTTTTATACCTTCATATCTCAACTGTGTTAAGC
WI-18119	38	T C ---	---	---	GCAATCTGTAAACAGTTTGGTAGTGGTATTACAGAGGATCJTTGTAAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAAATTTTGGTTCTT
WI-18142	66	T G ---	---	---	TTCAAGATAATTACAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAAATATCTATATACJ T/GJCCCAATAAATCACTACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T C ---	---	---	GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAGTCCATGCCTGGAGGTTAGTCTGGGGG GT/CJCGCGGGATGGACACACAGACACACATAGATCTGGCATCTGATAGCAGGGGCATACAG
WI-18244	35	G T ---	---	---	TCAATCTGAAAAACCTGCTGTAAAGCCAGCATGGGTGTG/JGGGAGGTGATTATGCGTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACACAGTGACAGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---	---	---	ACAGATGTCAGTTGTTGAATTGGCCCATTTAAAGTATGGGGCTTTCTTGTAAAAAGTCATCCAAA AGGCTTGGCAAGAGTTTGTCTATACAACGGAGGGACAGAGAAACATGA[G/A]CTGGGAGTAGGCTCT GACAGAGGTGGGGCTGC
WI-18261	26	G A ---	---	---	GATTTGAAGGGATTGCTTTATTAACTG[A/JTGAAAAGCGTGATAGAGGAACCTGTTTAAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAGATTG
WI-18268	88	C T ---	---	---	TAGGAGGGAAAGAGGAGGTGGCTGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAAGC TTCTTACTTCCCCCATAGATC/JCCTGACAATGTGCTGCAGAAGCCCTCCAACTGGAAC
WI-18299f	107	C A ---	---	---	TCACAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTTG[A/G]GAATTTCTTTGCCAAATTTATGACATATCTG CAG
WI-18299e	101	A G ---	---	---	TCACAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTG[G/A]GTCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAATTTATGACATATCTG CAG
WI-18299d	77	G A ---	---	---	TCACAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT T/GJATCTATTTGGGTCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAATTTATGACATATCTG CAG
WI-18299c	67	T G ---	---	---	TCACAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT T/GJATCTATTTGGGTCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAATTTATGACATATCTG CAG

WI-18299b	52 G A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACTTG[G/A]TTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAATATTGACATATCTCG CAG
WI-18299a	48 C T ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAA[C/TT]TTGGTTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAATATTGACATATCTCG CAG
WI-18307	76 G A ---	---	TCAAATTGTACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCGGCTG[G/A]TGCTATGTAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGTGGGTACTGATT TATC[C/TT]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18324	72 C T ---	---	ATGAAAGTCACTTCAATCATAAGGTCAAGAGAAAGAATGTTTCAGAT[C/TT]TAAATCTATGAAAA GGTGTATCTCTGCTGCAATTTAAGAAACAACAACAAGTCA
WI-18350	48 T C ---	---	TCTTGACATGATCTGTGAATAACGTGATTGTGGTTGAATTCCTGGAAAAATTTGAAGAATAAAATTG ATTATTTCAAG[G/C]TGTGCATTGGTTTATACATATCTCTCTCTCTTAATGCAAGCTATG
WI-18395	77 G C ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAACAACCTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCAATAATTCAAAAACAAGCAGCAGAATTTGGAGGATAATTTGTT
WI-18398	62 G T ---	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTTCGCTCTTTCTAAATTTAAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCACTTTGTACAAAGTC AATGAAAA
WI-18396	21 C A ---	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTCTTACTAGAGATTTTTTTCCCTTTAATCCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAAGCTCTGGGCCAGAGGCCCAAGTGCTA
WI-18409a	20 C A ---	---	AAAAAGGAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAATAAGTTTCTGG[C/T] TTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCCAAGGGAAACACAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18442	62 C T ---	---	TTGATGTTAATACTGTCAATTTGGAGATCGGCTAAAAAT[G/A]AAGCATAGTTATTATTAGCTTTGG TATATTCTCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAACCA
WI-18452	38 G A ---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAA AGCCCATATAAA
WI-18489	102 A C ---	---	CTGGTGGGAGGAAACAAATTTGGGTATATTACATAATGGAAAACTTTCAGAAATAAGAAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAAATCATTTATGCTGATGGAAAGAAACCAATTCA TAAGAATACACAGTAGAT
EST5b	93 A ---	---	

EST5	93 A	---	---	CTGGTGGGAGGAAACAATGTGGTATATTCATACAATGGAAAACCTCTTCAGAAATAAGAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAATCATATGCTGATGGAAGAAACCACTTCA TAAGAATACACAGTACAT
EST6	48 C	---	---	TTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAAGCTTTTCTCTTTTGCACAAGACAAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A	---	---	GGACAGGAOCTCTATCCCGCTGTGGTGCAGCAGCGGCTGATGGACTGAGGCCCCAGGGGACTGGGOC CTCTCTCAGGGGCTCTCAGGACCCAGAGCTGTCTCTGCTTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCACGATGGAGATTTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c	104 G T	---	---	TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACACGACCTAGAAAAGT GAGAACAACTCTCATTACCATCATGTATC[G/G]AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C G	---	---	TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACACGACCTAGAAAAGT GAGAACAACTCTCATTACCATCATGTATC[G/G]AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C T	---	---	CCAAAGTCTCCTGTTGCTCATAAAGAGTTTGTGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCTTCATTTTACAGAGGTAGCACAA[C/T]TGATTCCAAACAAAACCCCTTCCOC TTTTTAAATGATTTCTGTTCTAATGCCATAGATCAAAAGCCCTCAGAAACCAATTGTGTGTTCTCTT TGAAGCAATGACAAGCACTTACTTTACGGTGTGTTTGTGTTTCTTAT
WI-18746	114 G A	---	---	GCCAGAGCTGAAGTCTCTTTTCTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTGACTTGACCGTTTATATTACTTTTGTAATATTTCTT[G/A]TCCACATTTACTTCAAGT TTGGATGTGGTTAOCG
WI-19112	212 G A	---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGTTACGGCCAGGGGAATATGCCAAGG GACCCCTTAATGGAACACACAGATCAGTAGTGCTATCTCATGACAACCCACAAAGAACCCGACGACAA TCTTTTGGGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTCAACACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A C	---	---	TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTTCTTAGATCATGT CTCAATGGAACACACTCTTCTTACGCTTACTTGAATCTTGCCTATATAAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC[C/A]TATGATTAGCCGGTAACT
WI-19057i	175 G A	---	---	CCCATTTATTATAGCCAGTGTGCTCAAGAGTAGAGGAGCGTCTACTGGTCTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGTATGTACGTCAGGCAACCGCAGCCACTG TCTTCATGCAGGAACACAGTGGCCAGATCCCCACAGCTC[G/A]TCTCTCATCTTGGTTTGGCCACA

WI-20103	168 C T ---			TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAAGTGGGATGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCCA/C/TTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---			GCCTTACCCATTTTGCACATATACATATGCACCACCTTTCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA/G/ATTTGAATAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTTCACTACATCAGAGGCAAAATAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---			TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTTAA/GJACACTGTTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA/G/AAAGGGAGTTTCCACGACGCCAGTGGTGAGC TGC
WI-20613b	156 A C ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA/G/AGTTGGAAAAAGGGAGTTTCCACGACGCCAGTGGTGAGC TGC
WI-19984	47 A G ---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA/G/ATTAACATTAGAAAA GCAAAATTTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTCCACACTGGAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---			GCCAGTTGGAATATGGCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTCTCTTGGAACTCTGCACCGACTGTCCATGTCTGTGGGACCTTACACATTCAGTTTGACAGI T/C/JTGAANAACCAACTGGAGCTGCTTTTCCAGAATGTTCTGTTCCTTCAAATAGGAATCCATG TTATTCTTTCTTGGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ---			GAGTGCCATACCTTCTCCAGGCCTCTGCCCAAGAGCAGGAGGTGCCTG/AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGTCACTCCCATCCCGTAAGACCTCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ---			AGCAGTGGCCTTATTGCATCCCAACCAACGCCCTTGAACAGGCTGCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTACAGTCTTTTAAAGTGAATGTCGAGAAAGAGGACCCG/G/AGGAAGCCG TCTGGCGCCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGGAT GTCGTGGACACACAGACTATTTTAGATTTTCTTTTGCCTTTTGAACC

WI-20146	31 T C ---	---	TGAGTCTCTGTGAATTCATTGAGCAGTTAGCTTCATTTGAGATAAAGTCAAAAGTGCCAAACACATAGCTCTGTATTAATCCCATCATTAAGTAAAGCCCTCATTTGAATGTGAAATTCATACAGGC
WI-18922	74 G A ---	---	TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACATTTGGAGAGATGGCATAAACCCTGCTCACCCTGGACTTAAGC[G/A]TCTGGCTCTAATTCACAGTGCCTTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAGAGCCACACAGTTCTC
WI-18763b	53 A G ---	---	TTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[G/G]TATTTAGAATGTACCATATTTTTTGTAAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18763a	38 A G ---	---	TTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGA[G/G]TGACGATGATGTGAATATTAGAATGTACCATATTTTTTGTAAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18771b	75 A G ---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACTGCTCTCGGAGGATGCCCTAGAAAGATGTTGGGAAACAGAG[A/A]AAATAAACTGAGTTAAGGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACTGCTCTCGGAGGATGCCCTAGAGATGTTGGGAACAGAGAAATAAACTGAGTTAAGGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	GGGAAAAATTTGAGACGCAATACCAATACCTTAGGATTTTGGTCTTTGGTGTGTTGATGAAATTTCTGAGGCC[T/C]TGATTTAAATCTTTCATTGTGATTGATTCCCTTTAGGTATATTGCGCTAAGTGAAACTTGTCA
WI-18742b	51 C T ---	---	ACAAAGTCCGTAGCCCCCTCAACCTTCCCTGTTTTCACCTTTTGCCAAATG[A/C]TATCGGGTTGGTTTCTTGATTTATTTAAACGGTTGTGGTTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA
WI-18882	94 C T ---	---	GTCTTACC GTGTGTCAAAATGGGGTCTGCTCCTGCTACCTTGACCCCTCCCTTTCTGCTCTGCTCTCTCTCATCA
WI-19970b	167 G A ---	---	TCAATCCCAACAACATCCTCTGCCA[C/T]ACACAACAACAAACGTAAGTTTCATTTGGGCAAAAATTGAGC
WI-19970a	126 T C ---	---	TATAAGCCCGAGTCACAGGACGGCCTGTCTGECACACAGACAGGGGCTGCCTGTGGAGCCTGCCACCGGGCCCGGCAGTCAGTCACGGGGGAGGAGGCTGCCCGTTCTGCCAGTTCCCTCACTCGCGGGAGCAGCAAAAGGCCCTCTCACTGGGTTGGTCAAAAG[G/A]TAGTCACCTTGGCCTGGTGCTATCCACAGAGGATGTTGTTCAAAACAGAAATCTTTTAAACGACTGACCTTCCCTTAAAAACAGA
WI-19970a	126 T C ---	---	TATAAGCCCGAGTCACAGGACGGCCTGTCTGECACACAGACAGGGGCTGCCTGTGGAGCCTGCCACCGGGCCCGGCAGTCAGTCACGGGGGAGGAGGCTGCCCGTTCTGCCAGTTCCCTCACTCGCGGGGACCAAGAAAGGCCCTCTCACTGGGTTGGTCAAAAGGTAAGTAGTCAACCTTGGCCTGGTGATCCACAGAGGATGTTGTTCAAAACAGAAATCTTTTAAACGACTGACCTTCCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAGAAAT// GACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGCTACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTG/CJAGAAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTG/CJGAGAAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCG/CJCTGGCTG TGCACATTCCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGGTT CTCTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TAAATCCAGCCCTACCCCTGTTAGTTATTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGGTATAGTGGCCAAATAGCACATCTCCCAAGTTAAAGACATGGGATCATGAAAGT GCTGTTTGTCTTTGAGAAAGAAATATGTTTGAGCGCAGAGTAAATAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCCTCCTATTTTAA//CJTG
WI-18944	147 A G ---	---	CAAGGCAAAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAACAAAA AATGCCAGAAGGATAATATTGATTCCTCACATCTTTAACTTAGTTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC//GJTGTTTAAATTAATTTCAAAATATAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTCTTCTTCTTCTTAAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTTTTAAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATTACAACATAATTATTATGCCCTCTCTCACAGTCAAAAGGAAGTGGTGGTTGGT TTTTGTTGCTTTTTTAGATTATTGTCCTCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTTA AAATAAATAAATTTGGGAAAAGGTGA//GJACAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCACGAAACTGGAATAAGCCTTCGAAAAGAAATTTGCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTTGCTGATTTTGACCTTGATTTCAAGTTAACTGTTCCC CTTGGTATTGTTTAAATCCCTGTACATATCTTTGAGTTCAAC//CJTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAAGACAAAGTCTGTGGCTTG

WI-19042	193 A C ---			TTTGTGAGTGTGCTCTGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTAGAGTCCACAG ACACAATTTATCTGCGACAGAACCTTCAGCATTGTAATTATGTAATAACTCTAACC[A/C]GGCTG TGTTAGATTGATTAACTATCTCTTTGGACTTCTGAAGAGACCACTCAAT
WI-18984	208 A C ---			ATTGGCCCTGTACAGTTGCTTATTATAAATCATTAACACACTACAGGTGTTGAATGGTTAAAA TGTAGGCTCCAGTTCATTTTCAGTTATTTCTGAGTGCAGACAGTATTTCCGACTGTATTAAAT GTAACCTATTATGAATCAGAAGCAGTAGACAGATGTTGGTGCATAACAATATTGTGATGCATT TATCTT[C]ATAAAATGCTAAATGTCAAATTAACACTGCGCATGTTGACT
WI-18851	90 T A ---			GCCTCAATTGGCAGATTGATTGAGTGGCCACAATGTAACAGGGTGGTAGTTGTACTCATTTTGAAT ATACCTTTCCCTATTGTATTCTT[A]GTAAATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C]GGGGTAGCCATTGTGCAGTCATGCCCCGGGGAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---			ACTCCTCTGCTGTCTCCAT[C/G]ACTGTCTTTTGAACCAGGAAAAGTCACAGAGTTTAAAGAGAA GCAATTTAAACATCCTGAATCGGGAACAAGGTTTATCTAATAAGTGTCTCTCCATCACGTTG CTACCTTACCACACTTCCCTCTGATTTGCGTAGGACGTGGCATCTACTACGTACGTGGCATAAC ACATGCTGTGAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---			TGGAAATTCCTTTCATCTGGAAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGTCAGTA TG[C/G]CTAGGGAAACATTCATCTTGAGTCAAAAATCTCAATTCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---			CACGGTTCCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACGCCCTGTATGACCGCGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---			CACGGTTCCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACG[C/A]CCTGTATGACCGCGCAA ATATCCCAAAGCTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---			TTGAGGAGGTGGGTGAAGTGTCTCTGGCAGGGAATTTGTGACACTGCATTGCTGGGCTGTGTCTCQ[C]GGGCTCTCTGGACCTTGCAACCGTGGATACCAGGCCATGGTCAATTTGGTCTCTGGGAGGG TGGTGAAATAAGGC

WI-18972a	112 A G ---	---	AGGCTGTGGCTTATGTACCCAAACAGAGGGGTCCTGAGAAAGTCTGGCTGCTGGGATGCCCTGCCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAG[AG]TCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCTTCTGTGGCCACACAGGCACTACGGCTTCTCTCTCC AGATGTGCTTTGCTTGAGCACAGACAGTCAGCATGGAATGCTCTGGCCA
WI-19016b	184 C A ---	---	GTTTGCAAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCAA[CA]CTCAACACTATTGAC TTTTGGGCTGGATAGTCTGTTGTGGGGTTGCTTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTTTGCAAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC[CA]TGTATACAGAGGTTCACTCAAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTGTTGTGGGGTTGCTTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCAATTTATTTCT/CJGATAGAGACTGGCACAAAGCTTTGGGCTAAGGACACCCGGCCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGGCACTTACTTTTGAACGAAGTGGCATAAGCAACTCAGTGTGTGCCCC CTTAGGTGGGAGCTCTCC[C]A[CA]CTACCACTCCCAAGGATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCATATACCTGAATATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGGCACTTACTTTTGAACGAAGTGGCATAAGCAACTCAGTGTGT GCCCCTAGGGTGGGAGCTCTCCCCCTACCACTCCCAAGGATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCAGCTCTGTCATCCTTGTCTGAGGGTTCTGTGTTACGGCCCCCTCCAGGCATGGTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAGCCCCAGCTCTAGAGGCTCC[CA]TCAAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTACGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTCTCTCCCAATGCTCTCCCGGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCTTGCAGCCCCATTACAGGGGATGGAAGTCACAAGACATGAGT GGAGCTCATGCCCTCCATGAGGAGCCCTTAGTATGCTGACATCTGCCCTTATCTCTGCTCTCT CCCCAGTCTGTACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGAAC GGAAGGAAGGGCGGTCAT[CA]GAGGTGATGGCTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATACCTTTGTTTGT[CA]TGTTCAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTGGGCACTTGTGCAATATCTGGGCTCAAGTGGAGGCCAGGTG GGAACAAGGCCCTCAGAAAAACAAAGGACATGCAGCCTCCCTGAGCCAGTTCTCT

WI-19766b	93 A G ---	---	TGGCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGTCAGGACAAACAGAAAGGACACCAAGCCTGAAACCCCTC CGGACACAGCAGAGTTACAGCTGAGGGATGTCCCTGGAGTTCTGACCCATGAGAGGCCOCCCTC ACCTCTTCACCCCTCCTACCAACAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGACACCAAGCCTGAAACCCCTC CGGACACAGCAGAGTTACAGCTGAGGGATGTCCCTGGAGTTCTGACCCATGAGAGGCCOCCCTC ACCTCTTCACCCCTCCTACCAACAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTGGCTTGCATTGTGCGATTGGAAAAACCACCTTGGAAAGGGGACTTTCCTGCAA AACCTTAAGACTGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGAGC/GAAAGC TTAGAAAGGAACGAAATTGCTTCTTTGAATATGATTTAGGCGGGCGTGGGTGGGCTCACGCCT TATTAATCCAGGCACGTTGGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	CTTCTCTGTTGGCTTGCATTGTGCGATTGGAAAAACCACCTTGGAAAGGGGACTT/GJTCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAACGAAATTGCTTCTTTGAATATGATTTAGGCGGGCGTGGGTGGGCTCACGCCT TATTAATCCAGGCACGTTGGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGACOCCTTTTC ATAACCCCTTCTACATTGGAAGAGCACACCTTGTATACAGATGGTCCGTGAAGTCTTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACACGTAAACCAACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTCCAAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTGAAATAAAATTCCTATGGTCTTAATTGAAGTGTATGTTACTTCTTTTAGAATATCCTTTT TTCATTAAATAT/CJTAAACCACTCTATGTGTTCAACCTCTGTTTAAACATAAGATATGGGT TTTTGGAAAGGCCACAGTCACCACTCCATGAAGTGGCGAATGGTCTTGTGTTGGAAAGCTCTC CAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---	---	CCAGAAATAAGCCTGAATATCTCTTCT/CJTAAAAATATAATTTTCTCTTTGCTCTTCCAA GTAATCTTAAATGAACCTGTCTAGTCTATTTTATCTAGGCAATTATAACACTACCTAGGGGG TTTTTCTTTATACCTGTGTTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAGTCTTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCATTGTTAGCAGGA GGCAGGAAAGTGATCTGGGTCTCTGGCAGCAAAAGCGTGTGTAATATTTGGGTGACGTATGC ATCCCCATGCATTGGTTTGGCAGTCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60 T C ---				TTCTGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGT/CJGGA AACAGTAAAGCAAAATTACCACACAATTAGGAGGAATTTATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAAATTCTATTCATAAACCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 G C ---				TGATGGCAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTTCCCACAGGAGAACACTTGACTTCATTAAAGGCAAA[G/C]CTTTACTCTGTACTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACACAGATGCA
WI-20721	72 T C ---				CCTGCAATCACAAAAGTGGAACCTAGTTGATATTTTGAAATCATACTTGATTAAACCACCTTCAGAAA TTCTAT/CJAAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ---				CTGGATTTTAATATTTCTGGCTTAATAACCAAAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCGAAGATTCCCTAAGTAAGGTAATTGACGACTGAGACTAGTCGCGCAAA GTCATGAGACCCCTTAGCTGATCTCAT/GJ/AAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ---				GCTGCTCACTGGTAGCCAGCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTCGATGAAGAGACTGTTGGTCATGGCGGTGA/CJTGCTTCTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAAGTCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98 G A ---				GCTGCTCACTGGTAGCCAGCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTCGATGAAGAGACTGTTGGTCATGGC/GJ/AGTGACGTCTTCTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAAGTCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98 A T ---				ATTAGTTGCTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACAATG TTAAAAGGTACAGTAAAAATACAGTATTAT/AJ/ATCTTATTGTGTAGCACGGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTTGCCTT T
WI-19641a	46 A G ---				TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCAGTAG/AJ/TATTATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTTGATTTTGTTATTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGIGGTTTAAATTTTAAAA AATCTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 C A ---				ATATAGGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT/CJ/AGGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGTATGGACACAAGTTTTCATGCTATTA
WI-19673b	180 C T ---				TCTGCCATGATCACATTGTGATGAAGAACAATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT TACTCTCAGTGGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCAGTAAATCTAATAGT GAAAGGCCAAATGATGCTCAGTATCACTGTGAAAAACATTTTTC/CJ/CTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTTCCACACGCTCAAAAAACACAGCCC

WI-19673a	35 G A ---	---	TCTGCCATGATCACATTGTGATGAAGAACAATGATG/GJTCACACTAGTAGGTAACCTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGATCACCACCTGTAATCTAAT AGTGAAGGCAATGATGCTCAGTATCACTGTGAACAATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGCTTCAAGGTCCACACGTCACAAAACACAGCCC
WI-19724	35 A G ---	---	TTTATTTGGGAACAAGGATTGTAATTTGGTAA/GJCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAGCAACACGAGATTTGGTTTTCTCTT
WI-19307	196 T C ---	---	TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCCAAAATGGTACCCCTTTCAGCAAGAATG CAAGCCCTCTTGGATTGCCCTTCATGAGAAAATGGTGGCTGGGATGGAGGTGACATTCCTTGGCTGT GGTGAATGCAAGAAGAAACCAAGCAATGTATCCATAGAGGCCCTTTAAAGAGACCCG[T/C]JGG AAATGGGCCATGGTCTAATTTGGTGTGAATAAATAACCTCTTTGGCTG
WI-19269	85 A T ---	---	CTTCCCTCATCCCTCTTCCACCACACCACTCCCGGAACAAGTGTCCAGGATCCCTGCCCACTGGC CATTTTGGAGTGTGTC/A/TJTTGGTAGCAATGTGGAACCAACCCAGGGCCTTTGGGAGAAAATGG AGGGGTTGAGGAGTCCAGAGGGGCTTATTGAGGGCCTTTGCCACTTGTCTATAGCGGAGCTCG ATCTCTCATCATCTGGACAGGTGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122 C T ---	---	CAATGGACTGAATGAGTGCCTGGTGGGTGGGGCACACACACCTTCAATACACGTCAAGGTGG CTTCCAGTTTGAAGAACAGAAATCTGCATCTCAGCTGAGCGCACAGAGAGTJCTTCTTCTCTG ACCCAGAGCACTCAGAGCCAGGTCTGGTTTCAAAACTGCAATTAACCTGCGCCAGAGAGTTCAC CGTAGGCATCTTATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 G A ---	---	CACAGCATGGTGAATAGCATCAGATTGAATGAAGTTTGTAAATGCAACCAATAAATTAATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTAGGCCAAGTTTGGATCTGTCTGGACCT CAATGTG/AJCTCTCGGAGAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCAAACAGAAGCTTCTGAACCTCCTCTGGGAGGTAGCTGACAAG
WI-19076	40 G A ---	---	TTGGTTGGATACCTTGTGGAAGAAAAAGCAGTTTTTAATG/AJGTATTCAAATACCTTTTAAAA GTATTCTAGCACAAAGATTTTCTGTAACTAGATTATGTGTAACCTTTTCTAAATCTTGTAGGAG TGTGCGTTGTTAAGAACTAGAGCTTATCCTATTCCAAATCTATCTTGGCTCCTGAAAACTGCAGA AAGGCATTTGAAAGCTGTTTCTTAAAGATATGGGATTTCTTTTATCTT
WI-20218	26 T C ---	---	CCACACTCTGGTTTATAAGCTAT/CJAGGACAGAGCAGAGATGGAACCTGAAAAACAGGGTAG AAAAAACATAAATTGGAGGGGAACAGTGGGATGCAGAAAGAATGACAACAGCCACATGTGCCCA GTCAAATACCTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATCTGCTGGGGATCCTGCC ATGGATGCAGGAGAAAA
WI-20295g	154 T G ---	---	CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATCCCTCTTTTAATATCTCCAGGCTTGAATGGGAGGGCTGGGCTCTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT/GJCCAGAGAAAGCGGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTGCGCTTCACTTCTGTGACTCCTCATGCTGGGACTTGTCTTTGGGG

WI-20361a	192	G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CITTATGCAAGATGACAGAATATGTGAATCTGATTGTGCCAGAGTTACACTCTGCAGCTCCAAGCTA CAACAGTGCCACAGCTGAGAGTTCCCTATATCTCTACTACTGTGACAAATTTAGC(G/A)ATCCTTC AAATGGGAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCCG
WI-20572	75	A G ---	---	GAGCCAAACCCCAAAACAAAATAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTCTTCT TCAGAAAT(G/J)TCATAAAACATCATCTTTACAACATGGAGAGCGAGGTAGGCCATAATTTGTTCA AATTCATCTTTCTCAAAATTTAAAATTTGTTTAAATCCCAAGGTGCCTATTGAATCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G A ---	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTAAGTTGAATAATAGTATACAGCAATC TTCACTTTTTAAGAAATGTGAGATCCTTTGTTGGTTTTTATTCCTTAAGTACAAAATGCTAAAAC G(A)GGAGCCGAGCTCTCCGCATTCAGG
WI-20593	79	A G ---	---	TGACCTCATACTGGTCTGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTG CTGTACTTCAG(G/J)TTAAAATCTGGGAATGAGCATGCAGCAATGCTCCACAGATGAGGAAGAAA AGCTGTTAAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCTTCACCCAGACTAT CCAGAAGCCATTCATGGGTATTTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57	T C ---	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTATACCTTGTCCCTCAT(C/J)ATGTATCT TGTCCTGCTGCTTTTAGTTAGCAAGGTGATGAATACCTTTAAGTTTGTGTTCTTTTCCCTCGT GGTATCAGTGAATACTGATCTATCTCTGGCTAGGGTCAATTTACAAAATGGCCATGGAAGTGAAGC AAAAGGCCACGTTGGGATAAAATCACTCACCATCGAGCCACCCAGTATT
WI-19066i	239	A G ---	---	TGACAAGGGAGAGAGGGAATTCCTACTATTGCAAGGAATCCTCACTTAAGCTTCAAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCCAATCTCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGT ACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTA(G/J)TTCTTTTA
WI-19066g	184	C T ---	---	TGACAAGGGAGAGAGGGAATTCCTACTATTGCAAGGAATCCTCACTTAAGCTTCAAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCCAATCTCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTC(J/T)GGATGCTCAATTAC AGTACCAATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTA
WI-19066f	148	T C ---	---	TGACAAGGGAGAGAGGGAATTCCTACTATTGCAAGGAATCCTCACTTAAGCTTCAAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCCAATCTCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC AGTACCAATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTA

WI-19066e	147	G C ---	---	TGACAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCG[C/G]TTGGTCACCCGTGAGTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGGCTTCAGTAGTTCTTTT
WI-19066c	100	G A ---	---	TGACAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTGAGTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGGCTTCAGTAGTTCTTTT
WI-19066b	87	C T ---	---	TGACAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAAC[C/T]CTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTGAGTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGGCTTCAGTAGTTCTTTT
WI-19066a	72	C T ---	---	TGACAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTGAGTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGGCTTCAGTAGTTCTTTT
WI-20660	105	G C ---	---	TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGTGAAAGAAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTG[C/G]TTAATAAGGGAAGCATTAAATATTA CAGACATATTTACAAAGTTCTGAACATGAGTATCCATTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCCGCCCCAAATACTGTTTAAACAACACTATGTTTTTAAAGA CTGCTGCCAGCTTCTCTTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCTGCTGCATGTCATGTCACCCCTGGT[C/T]TTCGCTCCATCGGC TTGAAAGCTCTGAA
WI-18768	120	C T ---	---	TTCCCCAGGGTTCTGTATTGCAAGCTCAAAATGTA/GTATTAACTTCTAGTTGCTCTTGTCTTGG GTCCTTCTTCCAATGATGCTTACTACAGAAAGCAAAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTTAATGGCTGCAAAACCGGCAACCTGTAACCTGCCCTTTTAAATGGCATGACAAAGGTGTC AGTGGCCCCATCCAGCATGTGTGTGTCATCTTGTGATCTACCTGCTCC
WI-19087	37	A G ---	---	GAAAGCCAGAGATTAGCCCCGATTCCGCATCTGTCAACCAGGACAGAA/TTGTCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTTGGAGATCAGAAAAATTCATATTAAAGCAAAAGTGATACAAACA CAGTGATTTGGGAATGCT
WI-18790	49	A T ---	---	AGGAGGCTGTTCCAGGATCTGCCAGCAGCCTC[G/A]GTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGTGCTCCTAGGCTGGACAGGATTACAGAAAGACACACAGGCTGCACA GAAAGCCAGATGGACCTGAGTGTGGTCCAGCCCCCTACACTCAAGGCTGAGAGGGCCTCAGGAA AGTCA
WI-18987	35	G A ---	---	

WI-18919	26	C T	---	TGGATGAAACCACAGGGATTCCGGAC[CT]GCCAGAACCCATTTTATACCTCAGTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATACCTTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64	G A	---	CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATATTATATATGCAAGTTAAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G C	---	CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGTCA[Q]CJACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATATTATATGCAAGTTAAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T G	---	CTTCTGGTCAAGGCTTTGGACAT[Q]CJCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATATTATATGCAAGTTAAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19178a	170	G A	---	TCAGAAGCAGACATGGCATCTGTTCCCTGCTTGTGTTGTTGTACCTTTTACGAGACCTGAATT TTAGAAATGCCAGTCTGCCAGAGTGAGTGAGTGAATCTCCTTTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTATATAACATATCAACCA[Q]A/JTAGCATTAACCCATTTTATTCCTGTCTCT AGTGTCTGAAGATGCTCAACGATTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46	T A	---	CCAAGTTGCATCCATGTTTGATTTCTGATGAGACTAGAGTGACAGT[A/J]GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGGAATGCAAGCTGC ATAATTAAACATTTATCAAAGTCTCTTACAAATTTATTTCCGAGCATGTGAGTAAAGTAGACCCA ATGGGGAGAGAAAATGCCTGCTTCTTCCCTCTTTCTGCACCTGCCATAT
WI-19183	210	G C	---	CTGTTGAAGGCTTCTCAGGCCAACTCCAGCTTAAAGCCTAGACAGGTAAGGCACACATTTGGATG GCAGCATGGTTTCTCCCATTTTATGGCATGAAATATGTGGTTAGAAATAGGAACAAGCATTAATT CCTTTGCCAACAGCCTCACTTAAGAGGCTTTTGTCTGAGTCAAGCAACACTTGCCTGCTCTGCC CTTGGAG[G/C]TGCAATTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	T C	---	TTGAAATCCCAGTCTCTGGCCCCCAGGCAGGCTGTCAACCATAGATGTCTCTCTACTGGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGAGCAATGTTTCTTGTTATCTGAAACTGGAACCTGAACAGTTTGCCTTTCTCCTAGTCAOC AAGCATACTT[C]TCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	T C	---	GTCTCCCCAGAGTCTTCTGCACCCCCAGCCCTGTCTGCTGTAAAGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGCCCTTAGTTTGGACATGCTGGTAGGAGACTOCAGGGCGTG CACGGTAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCCATCTTCTCAATACAGCC[T/C]G CCCTTGCAGTCCCTATTTCAAATAAAATTAGTGTGCTTGGCTGTCTGT
WI-19135	20	G A	---	CAGTTACCCCTGCTTGGCTCTG[A/J]AAAGTGTCAATCAATTTGTAAATTTAGTATTAACTCTGTAAGAAT GTCTGTAGGTACGTTTATATTATATAAGGACAGACCCAAAAATCAACCTATCAAAGCTTCAAAAAC TTGGGAAAGGGTGGATTAAAGTACAAGCACATTTGGCTTACAGTAAATGAACGTGATTTTATTAACT GCTTTTGGCCATATAAAATGCTGATTTTACTTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A	---			TACACAGAGGGTCGCACCTTGAGCTCTGAGGGTTGGGTGTGGAAGGGGGAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCCCTTTTTCATAGGGAAGAGTGTACACCTCTGGCTATCTCAGGGGAATGGGGAAAAG AATCTTCAAGGGCAAAGAACTCGTGGGAGGATGCTGTGTATGTATACT
WI-19144	222	G C	---			GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTACGCCCTTGCTGACCTCCACGCCCTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTCTTCCTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTGCCTGGTG
WI-19139b	110	C A	---			CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTGGCAGACAACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGGTGTGCCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGGAAGCCACCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAATCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T	---			CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA[C/T]GGCAGATGCCCTGACAGAGAGTGGTGGCAGACAACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGGAAGCCACCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAATCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C	---			GGCTGGGACCTTTAGGAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGCTG[T/C]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173	A G	---			TTCAGGAGGTGGAGTTCGTCGAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCCCAGIATGCTCTGTATTTACAGCGATGCCCTCTGT CACTCATGCCCTGCCTAATGTTTCACAATGGTGGAA[G/G]CTTCATGTAAATGATCAGGACCCACG TCCAGTCTCTGAAAGTGTACAGTGTCCAGCCGGTTCTGCAGCACTA
WI-19222	179	C T	---			CGTTTCCCCTAACTCACCCAGTTTAGTTTGGGATGATTTGATTTCTGTTGTTGATCCCATTCTAA CTTGGAAATTGTAGCCTCTATGTTTCTGTAGGTGAGTGTGTTGGTTTTCCTCCACAGGAAAGT GGCAGCATCCCTCTCTCCCTAAAGGGACTCTGCGGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGGTACACTGACGTGTCCAGAAGCAGCATT
WI-19117	134	A G	---			AAATAATGCAACGCAGGAGGAGAAAGAAATGCCTAAGACAAGAACATCTCTCATAGAACATTG ATCTGTTTACAGGAAACAACCTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTTCCCTAAGACATTTTTCATTCATGAAATTTTCAAGTTTTCATCTGTACA CATTTCTTAAACACATGATACCAGCAGCACTGAAAATGAATGCCGAATTTG

WI-19134c	263	CT	---	CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTCACACTCTGCTCCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGCAAGGGGTGCAGCCCAAGGGTCAG GCCCTTCAGAGCCAGGGCTAGAGATGCACGGTGCTAGAGCCAGCTGCACATCTCTTTTCAGAGCAC TTCATCCACTTGCTCCTCTACCTCGGCACTGGTGGGAAAGGG
WI-19134a	162	TC	---	CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTCACACTCTGCTCCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGCAAGGGGTGCAGCCCAAGGGTCAG GCCCTTCAGAGCCAGGGCTAGAGGATTCGACAGGGTGCTAGAGCCAGCTGCACATCTCTTTTCAGAG CACTTCATCCACTTGCTCCTCTACCTCGGCACTGGTGGGAA
WI-19224	112	CT	---	GGTTTCACCACTTTCCCAAGGAACTCCGATGAAGTGTCCACAAAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTTTCATAATCCAGCAGGCCAGAGACTTCC AGGAAACTCATCAAGGAGGTGAAATGATGGATGACTCTCCCAAGATGAAAA
WI-19201	179	TC	---	GCAGCTCTAAGGACCCTGGCCATTAGCTCTTGCTTTTGATGGCATCTCTTCCACCTTGCTCTC CTTTGCTCCTCTGTGTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGGCCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACTTCCTGGGGATATAAATTCAAAAA GTGTGATGTGCTGCTCAGAAAGGTGAGACTCCATGTCTGCCTTGGCTCAA
WI-19034	45	TC	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAATTCACCTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTGAAAGTGCAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTTGATATACACTTCAGCATTTAAGTTCTGTCGAATTGAC ATTGCTACTTATAAACTTAGTCCCTAAGTCTCTTATGCTGTGCTATATA
WI-19102	25	CG	---	TGTTCTGAGTCACTGAGGAGAGCTGCTTCACTCAGGAGTTCATGAGATGATCATGATGATTCAT TGCGACGTATATTTCTTTGGAAACAGATGAAGCAGAGGAACTCTTAATACITTAATCGTTCT TGATTAGTATCGTGAGTTTGAAGTCTAGAATCTGTAAGTTTGAACCTCAAGGGAGAGGAT AGTGAATGAGTGTGAGCATCGGGCTTTCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	AG	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCAGTGGGGAAT/ GJAAAAGCATCTNTCAAGTCTTTTGCCAACTTTGGCTGC
WI-18548a	62	GA	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCAGTGGG[GJAJA AAAAAAGCATCTNTCAAGTCTTTTGCCAACTTTGGCTGC
WI-18700	97	TC	---	GGCAGCAGCTTTTAAATTTGAACACTTTCTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACTGAAATCTGCTGAGAGCAGAGCTTC/JAAGATCCACAAATTCGAAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121	CT	---	CAGAGGGAAAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGTTCTGTGT GCATGGAGGAAATCAGGGGCGCCGNACAGCTGAACCTTCGCGAGGACAGAGGGGGG[CJTGACAGCA GCGCATGCCACAACATTC

WI-18017	87	C A	---			ACAAAAGAAAATGGAATAGGTTTGGGAAACTTATCTGCATGTACAAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTTCATTAAATATATCTCTTTGCAT CAGAGCTGGTGGAAAATCAT
WI-18148b	101	A G	---			TTATTGGCTTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTTCAGAAACCCNTCGATTCTGAATATCC[C/A]GJGGCGGCATATGCAAGGAAGATGA
WI-18254	64	T C	---			TATACGGATCATGATTTGTGTGACCACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCACT/C GCCAAAATCCCTCTTGGCTTCTTGTAGTCAGTCTCTCCCAACCCAGGNACITGGCAACCTGTTT TCGGTTCCTAGACATTT
WI-18265b	117	C A	---			CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGACGGCTCTGGCCNCTCTGGGTCC AAGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTGGGTGGTTTCTTCAG
WI-18295	40	C T	---			ACCACACATTTGTTGAGAGCCCTATTGTGGAGAACAAACAG[C/T]TTGGAAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATTCCTTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64	T C	---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ C/GAGTAATTAACACATAATATTTTANATGACAGTGCAATTAATAACGTCCTGGGTAAGCCAGAG GGGAGGAGGGCGTCTTCA
WI-22585	56	A G	---			TTTATTTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGCGAGGTATCCTTCATTTGGCACAGCTGTATAGATTGA
WI-21155	36	A G	---			GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGG[C/A]GTCTGTGTAGAAATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---			GCCTTTGCTCTTTGCTGTCTCAGAGGCCCTCAGATGGATACGCAACTTCTCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG[A/G]GGATCCAGCAGTGAGATCAGGCGGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98	C T	---			GGCAGATTCAACCCATAACAGAGAAATACTCCTTATTGGAAACAAGGTTTTATTTTGATATGATG AAATATTTTGGAACTAGAAAGTAGCAGTG[A/C]TTGGACAACGTTGTAAGATATTAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTATTTTCCCTCAATTAAGAATGGAACATGT CTTAATATTGTAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C T	---			TGAGACCCTCCTCTCAACAAAGAAATCAGTCAGTTACGACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TTGTGCACACAGTACAGTGACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---			TCAGAAATGCTTTCCACTGCCCAACCAAGAAATTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTCTTGGAGGTGCATGACAGGATTAGTCTCTCTGTTT/CJCTGGT GCAAGTTTGAACCAGTGATTATGTACCATTTGCATCAGAGCATCTGTTCCCTGTCAGATCCCCACTAG

WI- 20561b	94 T C ---			CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTATG TACTTCAGATGAAAAATCCTTACATGT/C/GGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---			CGTTGCTATTAAAGATGGCTGTTTAA/GTAAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---			GCCTTCATTTTCTGCACCCACCCCTGCCACAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A/T/AJATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---			GCCTTCATTTTCTGCACCCACCCCTGCCACAGTTATGTTGGCCTTCAATATATGGCGTT/AJTAGAA CATATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---			GCCTTCATTTTCTGCACCCAC/C/GCTGTCCACCACTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---			AAAGATTGCAGTCTGGGACACAGTTTGGAAACACTATTATAAGTTGCACATATTACAAACAG NTCCCAATGGTGAACCTGGTATTCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGGC/ G/AJGTGAACATAATGTTTAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTGCTCTTTTATCCCTTTCAGGTTTCGATT
WI-21444	39 A G ---			CTGGGCAGCAAGTAACCAITTTAAAGAAATACTCTCAAC/GJAGTCTTTTTTTATGGGGTATTTC GTTGTTAACAAAGTTAAATACTATTATGGAACTAATCTTTGATTTTATTCGAGGAAGAAGAACTCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAACTTACTGGTCATGG GAGATTGGATAGAT/C/GCCTAACCTATCTCAATTTTAAGTAATGTAGCAA
WI- 22091c	205 G A ---			GGCGTGTATTGATGCAATGTCCAACCAAGTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTGAATCAATAATTC ATTACTGTGTCTGTAGCTTTTAAAGGTTTAAATGTTAGAGCTTAAGTGGTATTACTTGAGGGCA ACA/G/AATTACGGCTTAACAACACACTAATCATGAGGCTCAGGGATTG

WI- 21805a	45 A T ---	---	CAACTGCTGAGGCTTTCTACTAGCTGATTTATAATCCTATATTATJAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTTCTCAAGGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGGTT TTGTTGCTTTTGTAGCTTAAGCTTAAGTCTGTTTAGNAAATCCAGAGGAATATGATTAGGCCAGAGTTA CATTGGTTTCATAAAATCGAACAGTTGAAGGCTGTTTTGTAAATTGCTG
WI- 21778b	155 T C ---	---	AAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCGTAACTTTTTATTGAATTTATTGAC TCTGCCCGGTGTCGTCGTCCTTCAACTCCAGTCTGCAATGCCCTGTGTAGTGGGTCCCCAG GTCTGGGCTTCTGAGGTCCTTCTGGTAGAAGGAGGCGAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGTGATGAGGCGAGTTGGCTCAGCTGAGTCCCTGACTCCGGAAACACTGTGCCTCT CAAATGATCTAGAGCTCATCTTGGCGTACATGAGGGCAGTTGTTCTAGTACCCATTTAGCCCC ATGGCTCTTCAAGCCAATTCACACTGGGAAACACACCTCACAAGATGCCTATCCATTTGAGTTC ATACAGGTTTGTAGCTAGAACTAAAAACATTTTAA/CJAATTATCTA
WI- 21449b	222 C T ---	---	AACAGCAGCTCACTTCCAAATGCAAAAAAATTAACAATTTTAGAATAAAATTAATGTTTA TAATGCGGGTCAGAGANTTGAAGGTACAACAGATCAATCAGCAGCACTGGAGGCGGTGGAG AAGCCAAAGCCCACTGGTCAAGGGTCCAAAGTGAAGAAGTCCCACTGAGAGGCTCCACACCC AAATCATACCCCTCAGCTCCCACTTGGACAGAGCCAGTCTCTGGGTTAG
WI- 21558a	157 G A ---	---	GCTTACAGGAAGCTGTGACAGGCGAGNTGGGTGGAACCGACTCCAGCTGGAAAACTGGCCTC CCATCCCCCTTAGCGCTTCTTGGCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AAGCCAGGAGTCCCTTCCACAGATGAGGCTAGGGCTGCAA AAGGGCCCCGTGAAGAGAGATGTGGTCAAGGCTTTAIGGGTCTCTCCACC
WI- 22187b	178 G A ---	---	TTTGTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAAACCAAAACAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 22187a	110 C A ---	---	TTTGTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGGTGGCTAGCAGAGCTCATGGNGACCA GTCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA/C/AJCAAAACAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 21609b	146 G A ---	---	TCATGAATATGAGCCTCCATAATCTTCTCCCTTGTAAACAACTGCAGTCCGTTTCAACAGCTGTAAA AACAGCCCCAACCCCAAGACATCACAGAGGCAAGAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG/G/AJAGGGTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T	---	---	TCATGAATATGCAGCCTCCATAATCTTCCCTTGTAACAA[C]/GTGTGAGTCCGTTCAAGCTGT AAAACAAGCCCAACCCAAAGACATCAAGAGGCAAGAGTGGCAGTGAGAGGGAGCCTGT AAGGATGTTTCAAAGGAGGTCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G	---	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGTGCTCTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGG[AC]/TATGTGACAG TTT[C]/GTGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGG[AC]/TATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAAATGCTTGGGAATC TACGG
WI- 18829d	58 A G	---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[AC]/TTTCA TCATACAAGACACAGCAAAAAGCACCACCCATGCCTCTGAGGAACATTTGGACCATGACCCCTTGAAA AA
WI- 18829b	35 T A	---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGG[TA]/AATAACTTATGTGTACTTCTTGATTCA TCATACAAGACACAGCAAAAAGCACCACCCATGCCTCTGAGGAACATTTGGACCATGACCCCTTGAAA AA
WI-20964	87 G A	---	---	AGCCAACTAAGGCCCAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAAAGGA GCACAGGTAGTCCACAGAATA[G]/GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGGAAGAAC AGATGTTAACAAAAAATAAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A	---	---	CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAT[TA]/ACAT TGGCTGGAATGAGGTGGTCAGGAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T	---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATAGCGGGTGAAGCGGCTGCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCACCATCACCGGCCCTGCCCATCATGCATCCCAATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGT[C]/TGTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCACTCCCTGTGATGGGAATGAC

WI-21661	117 GC ---	---	---	GCCTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAATGTATAAATAAGAAATGACATTTTAAATAAATAA[G/C]TTTAGTCACAGTC ACACAAACTACCTTCTAAGGAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAG GA
WI-21980a	25 TC ---	---	---	TCAGTTAAACACATTCATCAAGGAT[C/J]AGATTAAATATGTCAAGTGAGCATAAAGGGAGATTA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTCAAGTGACTCAGGATAAGTTTATTAAATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---	---	---	TGCTTGATTAAATGTGGTGTTCACATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTTTT AAA[A/G]TAGCAATATCTATTATAATAATATTGAATAACACCATAATAATATCAGCTAAGGA AGTAATCTAATTGTGTGATTTTCAGAGGGAGAAAACATTACCTCTAGAGCTAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGTAGAACTAGGAAGGCACAGGGATTTC
WI-22457a	112 GA ---	---	---	TTGCTATAATTTCCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCAGCTATTAGA CAACAGATAACATACCTGGACACGGTTTCAGGCATGAAGGATACAG[A/C]CAGTTAATTAACATAAG GAACAGAGTCCCTGCTTCCTGAAGCATAGGATGGGGAACAGTAATGCAGATTAAATACCTGGGGCC AAAACCCAGTGAACCTACCCAGCTGAAACACTGAAGGATCTGGGTAAGGA
WI-21524b	97 CT ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACTTAT AATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACITTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 AC ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGTACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTCTCTGCAATGGACTATTTGCG CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACITTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT ---	---	---	TTACCTTCCAAACCCAGGCCACTTTGGAGAAAG[G/T]AAGAGATGCTATTATCAATAAGCCAAAGAC AATAGGGACTACCTGGGTAGACCAAGATGGCAGTCACCATACCATCATTCCTGCCACAGAACC TTTGACATGCTGCCCTCCTACTCGGCACTCACTGCTTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197 A G ---	---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC TGATCCCCCTTTCTCAGCAGCAGCACCATCTTCACCCCTCTGGGAAAGCAGCATTTGGAGCCTACACCA CTTGTCCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAA[A/G]G TGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTTGGGGGAAGAG

WI-21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTCTGCATCCCTTTCTCAGCACAGCACCATTCTCACCTCTGGGAAGCAGCATTTGGAGCCTACACCAAG/CTTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAGTGGGCAGACAGCTAGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG
WI-22663c	139 G A ---	---	CCCTTGTCAGTCTGTCCTCGGCTTCTCACTGCAGTGGCAGGTGAGCCGGCTCGCTAATCTTATCCAGTCTCGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACGTGGTGCACCTTACAGGC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTCGAATCCGTGTGAATGTGGGT
WI-22663b	55 C T ---	---	CCCTTGTCAGTCTGTCCTCGGCTTCTCACTGCAGTGGCAGGTGAGCCGGCGCTCTGCTAATCTTATTCCAGTCTCGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACGTGGTGCACCTTACAGGGCGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCGTAATCCGTGTGAATGTGGGT
WI-22663a	38 C T ---	---	CCCTTGTCAGTCTGTCCTCGGCTTCTCACTGCAGTGGCAGGTGAGCCGGCGCTCGCTAATCTTATTCCAGTCTCGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACGTGGTGCACCTTACAGGGCGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTCGAATCCGTGTGAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCTGCTGCTGCCTGAGTATTTCTGTAATATTG/CTTAGTCCATTTAGATTGTGTAATGATCTAAACAACCTAACAAATTAGTTTCTGTAATATTG/CTTAGTCCATTTAGATTGTGTAATGATCTAAATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAACTTTTATT
WI-22631a	52 T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCCTGGCTTCAGTTCGATTC/CTAGCACCATTTCAGGTTTAGGCAAGGTATTTAACCTCTCAGGCTCATTTTCTCTTTTGTAATAATTGTGATAATGGACC
WI-20258	157 G T ---	---	TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTTTAATCCACACTTTCACGAGGGGACAGCCCTGCCATGTGTCCTCCAGGCTCACAGCAGCGCGGTACTCTGCTGGTGGTTGGTGGCAGGTGGAGATGGTGACGCGCATTTGGAAACCCGTAAAGGCATGACAACGGAGGCCCCGGGGTGTTCAG/GT/CGCGTTGACGAGGTGCATGGCTGGCAGCGGCGCTCTACAGAAGGAGGAGCGCAATTCACAGCCCTCTTGAAGTAGTTTCCGGGGAAAGTACC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAAATCTAGGGTCTACTAAATAATCTAGTACTTGTTCCTACTCTCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAAGTCTGAAAGGATTCAAAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTTACCAACCCCA/C/ATJGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGCTCAGGGTCTGGGAAGGCCTG/GA/JTCTTAGAAGACATTACCCAATGATGAGAGGCGCAGTCGTGGAAGCCATAGTTTGGATGGCGAGACTTTCCGGCAGAGGAAATAGCAAGTGCAAGGGCTGAGGGAGAAATGAACTTGGGCTTGTCTACAGGTTGAAGGGCGCGGCTNTGGCTGAGGTTTAGTGGATG

WI-22724	117	A G ---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCATAGTAAGTCTGTAAGGGT[A/G]GTTATTCTATTTT CAAATCAAGATTGTCAAAATGTATAGTAAGTCTGTAAGGGT[A/G]GTTATTCTATTTT TGGGATAIGTTGGGAATT
WI-22750	48	G A ---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAGGAGAGTCAGCATCTTGACCATTCTGACTGTGCT
WI-22775a	60	A G ---	---	TGCTGTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTTGAATCCTTCATTCAGGCCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAC TGAGGTATGTAGGTGTTGGAGCCAGGAAAGGAAG GGT
WI-22808	143	C T ---	---	CTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCCAAAT ATC
WI-21016	207	G A ---	---	TCTCTGTGCTTGAGCCCTCATCCCCACCCCTCCAAAGCCCTCATGCCACCACACCCGTGCCACATT CCCCATCTCCCTGCTGCTGCCATCTCAAGTCCAATTCGAAGGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAGGAGGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGCCTGTGGGTC CT[G/A]TTGGCGTGGTATGTGGGGCCAACTCCTGAGGCCAGAGTTCA
WI-21031	31	C T ---	---	TGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCAATTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122	A T ---	---	CCATATCCAGTCTTTGAAGCTTTCTATTGACTTTTAGGGTCAGTTATTATCCCTTTATCACTAT GACTTTCATTTGATTTTATTTGTTCTCCATTCTCTGTCAAACITTT[C/A/T]TTTTGTTTATAA ACTGTTTCTAAACTTCACCTAATCTCTATCTGTATTNCTGTAGTCCCTGAACTTCTTTAGAGG
WI-21186	95	G A ---	---	AGCGAGCATCAGAATCAGCTAGAGGGTTGACTAAACAGACTTCTGGACCCAAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCCTAAGTGTTCAG ATGCTGCTTGTCCTGGGGAACACACTTTGAGAACTATTGTTCTAAATGTCTCTCTCTTTTAAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94	A G ---	---	CCACGATAACTATAAAGCAGAAAATTAGCTTTGAAATCAAATAACATATTAGTAACACACATT CATTTTATAACACACATAAAGACAC[C/A/G]GNTCTCAGTAATGCTCTAGCCAGGGTCTCAA AGTATGGCTTCAGACAGCCCCATTTCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---			TTTCCCACATACCAATGCACCTGTTGTATAACTATT/CJGTGGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATTAACAATAATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAGGTTCTCTATGGCAACAGTGATGACATTTGGTGTCTCCTCAGCAAGTC/G/AJTCCAAACCTTC CAAAAGAAGCAGTCATTTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAGGTTCTCTATGGCAACAGTGATGACATTTGGTGTCTCCTCAGCAAGTC/TJGTCCAAACCTTC CAAAAGAAGCAGTCATTTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 C T ---			GAAACGGGGTGCTAAACAAGAAAGTCTCAGATCCCACTGAAAATCTGTTTCAGTTTCACAGGCTC TCTCAGAAAATGCAATATGTACCAATTTGCATGTACAATTTTCAGAGCCTTCAAATACATTCGGGG TCCAATCACATACTTCAGGTTCCAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTT/CJTTCCTACTGAATCTGGGTGGGAG
WI-21122a	42 C T ---			TCACTTTGTATCATAATCCCTGTAAAGCTAAAGTTATTCA/CJTJTAACAGGAACCTCTGTTTTTC TTATTCAAATGTCAACAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGACAACCTGGAAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53 A G ---			CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGGAACCTATTCCACAGGAG/A/GJCAAGGAGAAG CTGTCTCTGG
WI-21054	23 G T ---			AAGGAACTGCATGGGTACAAATG/TJCCAATTCACTTAACAAGGTGGGAAACGGGTCAATTCT TGGCCTGCTCCAGAACAGGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---			GGGACCCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTCCCAGTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCT/CJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT
WI-21059a	63 C T ---			GGGACCCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTCCCAGTGGCTGG/CJTJ GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCCAGCTTCGTACATCTTAATTTCAAGCTG AAAATCCTGGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT

WI-20442	37	T C ---				TCCACGTTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAAGGTGGCACAATTTAAGAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	T C ---				GTGACAAGAGGTGAAGCAAGGGACAAGGGGCGAGGCGAGT/CJCTCGGGCGGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C ---				ATCAGAACTGCAATCTGCACATGAAGAACCTGGGGGAATGCCTACATCTGGAAAT/CJCATTAAC ATCAACGTTAAATTTGTCCGACCAGTTCTTCAATGCTGATCATTGATAATGACAGATCCAACAT GAAACTCCTGAAGCAATGAATATTACCTTGCTTTCATGCAAAATTAGGACCAAACTCAAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTTGACAGGGATCTCT
WI-21149a	167	G A ---				AGGACCTGCTCTCACACGTTCCCTCACCCCAACAGCTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTAAATTTTAAACAATGACCTTATTTATCTTTAACTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAGCTTTTACAC/GATGCTTCAGAATGCGGCGAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188	A G ---				GGTGCAACTTGGAAATAATGGTTTAAACAGGATAAGCATTAAAGGAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGTCCTCGGTGAACCA GACAGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/GJGAAGTGATTTCT GAACTGAGCAGCACTCATGTCTGATGGGAACTCTGGGAGAGAGCCT
WI-21382d	125	C G ---				CCATTGCAGTCCAGAGATGAGAACTGGACAGAGGCAATCATGAACAGAACGGAGTCAAGAGA AGGGGTTCTAAGATGGAGAGTGGGGGGGTTTGGATCCAGTGGGATNGGCTTCC/CJGAGGT GCAACCCAAAGGAAGTCTCTGGAAGCAGCACCAGTCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAAGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGAC
WI-21437a	201	G A ---				TCCGTAGGTTGGAGTCTAGCATAGTCCCTCCCTCAAGAGGGACAAGGGTCAAGGGGCGAGAGC AAAAATCCAGTCTGTTCAACCGGAGACIGCTTTGGGATGGAAGTTCTGGAGTCCCTCCATT CTATTCTGTGGGCGAGGACATGCCAGGGCTGCTGTTAAATGGCAGGGTCACTTTACCAGGGGQ /AJCAGGCATAGTGTGGCCCTGCTGCTGGGGGCCACCCCTGGGAACAGT
WI-21202b	156	A C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTC/JTGA GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTTAAGTAACTGATTTATGA AGGAGGAGAGAGTTGACCA/JCJGCTACATGCATAGACAGTCTCTAAAGCGTATCTCTCAAAACATG A
WI-21202a	61	T C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTC/JTGA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTTAAGTAACTGATTTATGA GGGAGGAGGAGAGAGTTGACCA/JCJGCTACATGCATAGACAGTCTCTAAAGCGTATCTCTCAAAACATG A

WI-21627b	153 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATATTAACCATATTTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCAGTTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAACCATATTTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75 C T ---	---	---	GGATTTGAGTCCCAACTTGATCTCAAAATTCACCTTCTTGATGTAAACAAGCTCATTCCTCTAAAGTT TCAGTTTC/TTTACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTCCCTAGGACTAGGTAGGATCTCTCTGCTTTCTGCC TTACCTAGGCATAGTGCTGATAGCAGGGCTGAAGCCCAATTCATACTTGT
WI-20329a	68 A ---	---	---	CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGGTGCACAGACACAAGACATCAAT C/G/A/TCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCCTATGAGAC AGCAGTCTGGCTTCTTAAACACAGTAAACCAATCAAAAGAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	---	TTCTGGCATTCAAATGTACATGTAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAAGAACATTATAAAGGTAATT AAAACCTAGGTGTATACTTAT/CJATGGAACTAGTTTATTCNNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTTAAGGAAATTATAAACATTGAGA
WI-21504	147 C T ---	---	---	TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCCATTAAGAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGGCACGGCCGTTCCGCTCCAGCTGGGTTTTCOC AGATGCAACAATTC/TCGGGTTCTGGCTTCTCCACTGGTGGGGATGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 A ---	---	---	CTGCACCCAGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACCGGGGCAGGGAGGGGCAGAGAA[A/G]CACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	---	TAGCCCTTCTGCCAACATCTGGCAATNTAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCACTTGTCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGGCTCTTTGGAGAAAGGCA[A/G]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCTATTCTCCCTCCCTGAAG

WI- 21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTGATCTTCTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGACCTGGCAGTGGCTTTGGAGAAGGCAAAAGGCCACAGCAGCAAC ACTAGGAGCAAGACCTTCCCGTTCTCCACCCATTTCTCCCTGGAAG
WI- 20893d	207 A G ---	---	TGTTTGTTCCAGCCACATCTTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTACTGAGGAATACAATATTGTCACGTAGTTCATCACCCTGCTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTCAGIACATAACATTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI- 20893c	179 T C ---	---	TGTTTGTTCCAGCCACATCTTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTACTGAGGAATACAATATTGTCACGTAGTTCATCACCCTGCTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTCAACATAACATTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI- 19941c	71 C G ---	---	GAGCTCAAGGGAAGACCTTACCCAGATAGGGACTAACTGGAGGGTGGAGGAAACAAGGTGAAA GGTATTC/GGGTCTGTGAGACAAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTGTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGGACATTTCCATTCCAGTGCATGTCCCTTAAAT AACTGGGTACAGGACATTNTGGAAGGAGAACCAAGGACAGAACAAAGCG
WI- 21552b	166 C A ---	---	TGGGTACATGGACAGATGTATATGTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCTTCCCTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTATACCTTGATTATTTAAAATGTATCAATTAATTTATTTGAATTTAGTTACCCCA ATTGTGCTATCAAAATATCAATCTTATTCATTTCTTTGTAACATTTATTTGTA
WI- 21552a	66 G A ---	---	TGGGTACATGGACAGATGTATATGTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCTTCCCTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATACCTTGATTATTTAAAATGTATCAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATATCAATCTTATTCATTTCTTTGTAACATTTATTTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATATTTCTGTCTG/JTAGAGAGGA AAGAGCTGGTGCCTGCTCTGGAGGCAACGTCCAGTCCGGGAAAGGCACCTCGTGTGTGTCTGTCTC TCAGTGATGGGAGGTCTCCACTCGCCCAACAGGAGCCTCGGGCCAGAGATGAGAAATGCTGTAA TCCAGTACAGGGGCTGCTGCTGGGGTCCCAACAGCTCTCTTTGGGGG
WI- 21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACTCCCTCAAGGAGGACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGAATCTTTAATTTTATATCTCTCTTTAATACTGTCAAAATACACCAATA CTTAGAGGAAATAATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCAGTGA[G/A]AGTAG TATCTCTACATACCACAGTATACAATGATGCTCTCTGAGGTTTAGGAAC

WI-21514b	133	C T	---			TTGAACCTCTGAAGGTGGCTTATGTCCTGACTCCTCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGAAAGGAGCACATTACCATGGAGC[C /TACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCTTATGCAGGAAATAAATGAGG ANTTAAGGCTCAGATGGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-21514a	100	A G	---			TTGAACCTCTGAAGGTGGCTTATGTCCTGACTCCTCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCA[A/G]TCTTCAAGGAAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCTTATGCAGGAAATAAATGAGG ANTTAAGGCTCAGATGGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27	C G	---			ATGAACATGTTGCAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAA AATCCAAATGATCATTCTACCTGTATGAGGGTACTT
WI-19576a	113	A G	---			TTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAAATTTAACATT[C/A/G]TCTAGTTCAAGTATTAGT CACAGAANTTAACATCTGCCAGATGTACACAATTTGGTAAAACTACAGCTTCTCTCCACGGGA G
WI-21695a	141	A C	---			ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCACCTTGGAAAGTACTACACATGGCAATA AGCAGCCTATCTCTTTACCAACCCAGAAAGTTCTTGGGGCATGTATGGTAGGCCAGACCCCTTTCCAA GGGAAT[A/C]TACTACACTAAGCCTACACTGTACTGTGAGAGTCAATGTGGAAACAAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCAGCAT
WI-21574a	235	C T	---			AAOCCAGAAATTTAGGTACTTTGTATTATGAGGAACTCACTATACTAGGAAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCACTTTCCACTGATCCCTGGGAGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCTACTTCTCTCTGCTGTCAGGTGGGA
WI-21644c	151	T A	---			TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTTAACCTTTCAGGAAGCTTGGGT GTGACCCACTGCATAAATGGATTTTCACCATANTATTAAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAT/AJTTCAATCAAGATCCATGGAATGATGCAGTTTAAATGTGTCTCAGC TTGCCTACTGACCACCTTTCCTTTCTAATATGGCAACAGCACAGCAAGTC
WI-21614b	55	G A	---			TGCTTTAACCTCAAAAGTCCAAATAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI-21615b	151	C T	---			GACCGAGAAAACTGCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTACATATTAAGATAAGGATGGACT CTTCACTAGTATTATC/TJAGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATCTATATTGGCCAAAGGGAAAGGTAGGATGGGTACTGTGGAACGGA

WI-21981	61 T A ---	---	---	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATCTTTGAAGAAAAAAT/AJGT CTCCCTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATACAAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTGG
WI-21660	120 C T ---	---	---	TCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGGTGAACACGCCTCTCCACTGCT TACTGTGTATCCAAAGAGGAGAAAGCAGCTACCCAAAGCCTAACCTGGCC/C/TJTGCTCTTTTCAG GCTTCTCAGGATGCCACAGACATACCTGGGGAAGTGGGATGCAGGGAGAACAGGGGCTGTCTTC AGGAGGGTCAAGC
WI-19105c	211 C T ---	---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAAATATTTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAAGGA CACTAAGGCACATGGCTGGTATCTTTGCGTCAATAGACACGGGTAGCTCATGGTGAACCTCCTCTT GTCTGAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTCCCC ACAACTTC/C/TJTCAGGGGCGAGGATTTCCACCAGGGCCAGGGTGCCCCG
WI-19105a	33 T C ---	---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAAATATTT/CJGTGGTCCATGTGGTTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTATCTTTGCGTCAATAGACACGGGTAGCTCATGGTGAACCTCCTC CTTGCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTC CCCAACTTCTCCAGGGGCGAGGATTTCCACCAGGGCCAGGGTGCCCCG
WI-21760c	81 C A ---	---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGCTTCTTAGCTTTACAATAAGNGGAGG GACCTCTGACTGGA/C/AJCCCTCTGCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGI/GJGGTGTCTTCTTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCAOCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	---	TCTGCCATATTGTTCCAGCACCACCTATTACTGTTATTATTTCTTTTGAGGAAAAACAGGNATTAAAG AAATCTGTTTGAATTTCCATGATGCTAATCTATGTTTAAAAATCCTTTCTTACCAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTTGCAGAAATTTATCTCTAC/T/CJ AGAGACAATTCATAGTTCATAATCTTTCAGGGTTGTCTTACTTGGGGGGC
WI-20934a	72 T G ---	---	---	CCAACATGCAACATAGTCTTTCATTCTTAAAAAGTACATAGTAAAGGTAGAAAAACATTTGATTTCA GAGAA/T/GJTCTAAGACAAATGTCAAAATATTCAAATGGCCTGGCAGTGTGGTAATTCAGCAGAC AAACAGCATGAGAAAAAGCGGGAGACAGTAATAAATACGTGCCCCATTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCCAGGAGA
WI-21561	55 T G ---	---	---	TTTCCATTTTATTCAGCCGGGCCATCAGAACATAGCATCTATACCTTCGAAACCTT/GJCTCTTAAC CTCTCCAGGGCAAGAAAGGAAAGTATATTTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGTATTAGTATAAGAGGGCTTGAATATAATGATGATAAATGGTAGCCTTTCTGGA AATAATTTTGTGTAATCTGTTAAAAAGATTTTGGATGCATTGTCCCA

WI-22082b	67	CT	---			CAGGACTTGGTTTGTGCTCCCAACTGCACATAAATGTCCTTTTGTGTTGAGTTATTGGTTGTGTG[C /JGTTTTCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTCTGCTTTATCCGGATGACGG AGGTACACGGGGCGTCCGCTCAGTCCCGCCGAAGACGATTCGCTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAACTCCTCTTTGCTGCAACCTCT
WI-20993	139	A G	---			AACACAACTCCATGCTTTCAAGATTCCACACCCAGATCACTAAGACATATTAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAAATAACACATATAGCAATGATACAAATTAGGGGAAAAACCCCTGG GCTTCT[A/G]TAACAAGTGAGTATACATTAAAGACAGATTATGCAGATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAGGTCTTCCTAGCTCATCCACACATCACC
WI-21723b	125	A G	---			AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAAATAATTTTCTGAAGATAACAATT TGGACTTTAAAGCTCGACATAAAATTAGTACTTCAAAAGGTTAGTCATATTCCTCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	G A	---			AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAAATAATTTTCTGAAGATAACAATT TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGTTAGTCATATTCCTCAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	T G	---			CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGATATCTTCATGTTTC AAGCTTTAATCTGACTTGCTTTTACTATCCTTT/GJCCCCATTTCTTCTAATCTCTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCTTCTAGTTAATGCTGCCCCAAACA ATACTAACCCATTGAAGGATACTAIGGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	A G	---			TGACAGATCACACCACATTTTGTGTGTAACCTTTCTCCTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACATGTGCACACACI/GJAGAGGCAAGTACAAAAATGTAAAC CCACCAAAGTGCATGTGAATGAAAGTGCAAAAAGGCTTCATTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C G	---			CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTCTGCTGGAAATAACTGAAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATCAAAATATTTTCACATCTCTCTGCCAGTTAAACGTGCGGTGG CT[G/G]CAATACACACCAAGCCAAAGCGTAACCTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	G A	---			AATGAAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCAGCTTGTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG[G/A]AATTTACAACCCACTGAACATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAAATAGGCATGGGCAAT

WI-21079a	50	G A	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTG G A CGCAAAATCAAGT TGTTTAAATACCAAGTGTGCAGCTTTGATTCTCCATGAAATTAAGCTGTGTTGCTCACTTGTTTACA TAACTCAGGCCACCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45	T G	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT G JTATATAAACAGTCAATTGCT TGGTAGAATCCAGTCTGTCATTAAGTTAGCTCTAACAGTTAACATTGAAGCTTATACCTTATATTTA AATGTTAGCAATCTCTACTACATTTTCAAAATATAAATAATTTGGTTGCAAAATCCAGNAAGGGCA TTAACCAACATGGGACTGATCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79	A G	---	TGGAGTTAAGTGGGCTCTGCTATTTCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCGAGAGT GAGGGCAGAC A G GGATGAGGCTCTTCTGTAAGTCCAACAGACGCTCAAGATGCTGGGAGGCT GGGACTGCCAGGTTGGAGCCTCAOCCAGAGAGCCTCACTGCATTGACCCACACACCCACTCAOCC CAGCACAGGCACACGCGAGGGCACAGGCACACAGNTGCACTCAOCCGC
WI-18916b	42	C T	---	AATGGCATCCCTGTCGATACCAAAACATCTTCAGCAGCTCAGC G T GGCTTCCACTTCTTGGTACCC GGTTAACTGOCAGGNGGTGACAGTGATGCCAGGGCTGCGCCACTACTGCACTGGACACAGCCTCAOCC AATGCCACCTTCATA
WI-18916a	35	G C	---	AATGGCATCCCTGTCGATACCAAAACATCTTCAGCAG G C G CTCAGCCGGCTTCCCAC T CTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGATGCCAGGGCTGCGCCACTACTGCACTGGACACAGCCTCAOCC AATGCCACCTTCATA
WI-19828c	200	A G	---	TTCCCTTCTCCCCAAGTAGTGGGCAGAAAAGCTTTGTTAACTCTCTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTCTGTAGCCTAGTGCCAGGNTCTCGGCCCAATCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTACTCTTCTCTGACCTCACCACCACCCAAAAAT A G CTTTTAATCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C T	---	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTG C C T G AGCTGCATGCCACCCCTC ATATCCACCCCATCCACGCTCTCTGCCCCGACACCCACAGGCTCCCTGCTCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTCTTGATCCAACCCACAGCATCT
WI-19860	51	C G	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG C G CTGCAATCAGTAT CTCCCATCCACATAATTTCTGTTTGATTTTGCCATTCACCCATAAATGTTGGGATCTACCTCCCT CCTTGCAAAATTGAGCTGGNCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-9889b	80	C T	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGG C T TACAGCAATTTATTTCCCTCTTTCACTCCCTGTTAGCTTTGGTAGTGGCTGAT TTCTCTACTGATAGTTCCCTTGGCCACAGTCGTAAC T ATTCG

WI-19891c	172 C G ---			TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATGCTTGTGGCCCCCTCCCCCCCCG ACTCCTCTGTCCTGGGAAACGTGGCTTTGNTCTCCAGACACAGTGTGACAGTCCAGCTCTCCTCAGCGG AGCTCCCGGATCCCTCAATTTGCCATCTGCTGACTC[C]G[GTCTTCCGGGGCGTGGGGCGTCTTGT CAGGCAGCGGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---			GCACCTGTAGGGGTGAGCTTCCATGGTTCTCCAGCAGCGGCTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGG[C]TGGCAAACCTGCTTTGAGGAAATNTCCCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTACCATACTATGGAGATAACAGCTAATGAATGGTGGCAGAGCTTGGCCGTGTGA GTCCCCAGGGTAAAGTCTCTCTCTGTCAGTCCAGTCCAGAGCAGACTTCTC
WI-20270b	91 T G ---			AGCCATACAAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAGTGTACAAT ACATTTCATGTCCAGGATAAGGAGCA/TGACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGTGATCTTGTTTCCCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20270a	53 G A ---			AGCCATACAAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCG/TJTCAGTGTAC AATACATTTCATGTCCAGGATAAGGAGCATACACAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGTGATCTTGTTTCCCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20622	130 T C ---			CCACTTTCAATATTTACAAATGCTCAGCAGCAATATGAAAGCTTCAACACTTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTCATATACATCTTTAATGACATCATTTGCCAATACATA CATTATTTCTNTAACTTATTTTACAATAAGCCCAACATCTGTCATGCAG
WI-20768b	190 C T ---			TTCCACTCAAAACTCCACCCCAACCTTCTGGAAGGCGAGGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACTTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAGNACAGCACACATACTGCTGGGA[C/T]CAGGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-20768a	71 C T ---			TTCCACTCAAAACTCCACCCCAACCTTCTGGAAGGCGAGGGCTAACAGGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGGCACCCAGAGNACAGCACACATACTGCTGGGACGAGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-21909	153 A T ---			TGTTTGGCTTTGGCCAGGTACTCTACTGCTTTACATAAATATCTCATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAGGATATTTGTTGTCATCTTTAAAGAAA TGCTTAACATACCAAAAG/TJAGTGGGAATCAATAGAATAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATAGGATACCACCTAAATTTATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---		TGTTGCTTTGGTTGTTTCTTGGAAACATATTGGAACACATTGTTTTCATAAAGCTGTCTGACAGT GGCACAAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCATTATGAATCTGAATTTCT[A/G]TTAAT ACTCTGGTGCAATTCATTTCATCTGCAAAAGCAACTGGCACAACTCCCTTCCGGTGACAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---	---		CCAAGGATGAAATTTCCACATTTATTTNCITTTATGTGAATAGAAAATGGCAGTGAAGTGTCTCTATG AACTGAGCGAGGAATGGGCATGGCGCTGGGTACCGCTGGACGCTTGTGCTTCCAAAGTACAC TATGTGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---	---		GGGGAGGCATCATAGAAAAAACCCCTCAGCCAGAAAGTTAGGACATTGTGATCTCAGCCCACTAAOCA GCTGTATGACCTTGGTCACTAGGCCCTCTGCAGGCTCTGGTTG[C/T]TCATTTGCAAAATAAAACCCA GACCGGGTCATCTTTTCAGTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---		GACGTCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCCCTTAAGCACCG GCCAGTAGTGGGAATGCCATGCCATGGGTAGTGGGATCTGGGGGGTGCAGGACCTTGCCTTT [C/T]TTCCAATCTCTCTCTTAGCCAGAACTTTCGAGAGCCCCCTTNAATTTCTTCCCTCTATTCC CCTCCTTCCCAATGIGCTAAGTCCCAATTCAGACCCCTCCAG
WI-22292	53 A G ---	---		CCAGTGAAGGGTTACAGCCATAGTAGGTTCCCCATTGCTCAGTACCAGAA[G/G]TTTGAGTAC GGTCGTTAAAAATACTATTCTGACCACAGTGGAAA
WI-22387	186 C T ---	---		ACCTTGACACACCTGCCATCCGGTGCCATCTCTGGCTGGCACATCTATACCCTCTGGCTCTGAAAG GCTTGTAACCAACCAAAATGGCAGCTGGGGCTAAGGCATATTTAAACAAAGCTCCAAAGGACCCCTT TCATTTGGGTCTAGCATCCAGCCTCTCTCAGCAAGGAGGATTGTGGT[C/T]CCTTGTGTTTCTG AACAGGGCCAGGGCAGCCAGGCATGCCATCACTGCAGCACTCAACCT
WI-22395b	127 A G ---	---		GCCGTTCCAGTATTGATAATAATTTGTGTTAATTTCTATACAGAAATGGTTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAGGGGGCACTCTTTAAT[A/G]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---		TTTATGGCTCCTGAGTGCCTTACCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67 T C ---	---		CCCTTCTGGACAGTTTGCCTTATGTGTTTCAGACAATCAAGGNTCCCTTCCAGGCACAGCCAGTGC[T] [C]CTGGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCAAGAT
WI-21342d	59 T C ---	---		ATTTTCCCCTTCTGTGTTTCGATTTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT[C/T]TGGAA ATCTGCATGATTAAATAACATTAAACAGTTTCATAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTTAACCGAATGCAAAATAGGTATCCCTCAAAATTCACATCTCCTCCTAGTT T

WI-21763b	154	A G ---	---	CATACCCCTTTTAGTGCCACATTGATCTTAGTTAACAGTCTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT[A/G]CAGACATTGCCTGTGCTTCTACCCACGAGCTGTCTAGTGCACCT GA
WI-21763a	135	T C ---	---	CATACCCCTTTTAGTGCCACATTGATCTTAGTTAACAGTCTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/C]GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCACGAGCTGTCTAGTGCACCT GA
WI-22440	64	A C ---	---	CAGTCCATTTGAGTCCCAAGTCGAGGGTGCAATCTTCTTATCTTGTCTTAAGCCACTTGGGT[A/C] TCCATTCAGCTCTGCACCTTCTCCAGTTTCTCATGTGCAGAGTCCCTGGAGGGAGGCTTCTCTGG AAAT
WI-22449	74	T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT[C/G]GAAAAAATACACAATGGGAACGTGACA
WI-21965a	112	A G ---	---	CAGGTTCCACCAGAGGCTTTATTTACGCCACTCAGGACCCCTGCTTCTGCTCCAAAGGCAGTGAACA CAGTCAGGCTCTCTAAACACTGGCAGGGACCTCCCCACAGCC[A/G]CCCCACAGGGTCTCTGTT TCCCAAGTCTGATGGATTCAGCAAGACCTTCACACATTCACCCACTACCTGCTGGAGAGGAGGGTCT ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115	C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAAATTAAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCCTAGTCAGAAAGTCTCATGGACTTCTTCTTAAG[C/G]TGTTCTATGATCAGAC CACCTCTAAATGTGGCTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149	T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAATTTTCAACACTATTGACTATACAGAG TCTTCAATCCAAAAACAGTTAATAGTAACCTTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTCAGTAACATAAT[C/JAGGNTCCTGCATCTCTCTCACA
WI-22250b	132	C T ---	---	ACTTGCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATGAGTGGTTATTATGGGCTCTCTGCCCTCTGCTGCTGTTATG[C/T] GGANCCAGGAGTGGAGGAGGCCGTGGAAATAGACAGGGGAG
WI-22250a	89	G A ---	---	ACTTGCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATGAGTGGTTATTATGGGCTCTCTGCCCTCTGCTGCTGTTATG GGANCCAGGAGTGGAGGAGGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192	G C ---	---	GCAGCCATCCTCTCTCCAACACCTCCCAGGCCACCTTGGGGCCAGAGCACCTCATGCCCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCCAGGTTCTGGGCTCTCAGGACGTCCCAGCAAGTGGGA GCCACAGGTTTGTCTGGACTCCCAGCCAGGGGATGAGGCCAGCCCCAGAACTG[C/G]AGTGTCTTC TTTGACGGGGGCCCGCTGCTCAGCTGCTCTCTGGGAGGTGAGGAAGGAGGT

UTR- 04932-2a	149	C T	---			GCAGCATCTCTCTCCAACTCCAGGCCAACCCTGGGGCCAGAGCACTCATGCCACGACGAC CTACGTGGCCGAGTAGCGACCCGCTGGCCACAGTTCTGGCTCTCAGGACGTCGCCAGCAAGTGGA GCCACAGGTTG[C]/TTGGACTCCAGCCAGGGGATGAGGCCAGCCAGAACCTGGAGTGCTTC TTTGACGGGGCCGCTGCTCAGCTGCTCTGGAGGTGAGGAAGGAGGT
siFIBb	412	G C	---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACCCAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCGAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siFIBa	341	T C	---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACCCAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCGAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siGLV2	61	T C	---			GTGAGGAAGATGGACCTGGACAGCCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CTGACTCAGGACAGGTGACGCCCTCCAGGGAAGGGTCTTTGGGACCTCTGGGCTGATCCTTGCTC TCTGCTCTCAGGCTCACCGGGGCCAGCACTGACTGAGTGGCATGT
siSG1001 7c	70	T C	---			GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTGTGGGAT TAATCJAGGATGAGCCCTCCACACCTGGACACAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACCTAAAGTATGATGGCTTACTTTCTAATCC
siSG1001 7a	33	G A	---			GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGC[C]/AJATCTCCACCTCGACCTCCAGGGTGTGG GATTATAGGATGAGCCCTCCACACCTGGACACAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACCTAAAGTATGATGGCTTACTTTCTAATCC
siSG1002 3	63	A T	---			TAATGATAATTAGGGCATTCTCCACACGAAGATGACACAATTGACCCCAATATCATTGAGGC[C]/J AACAGTTGGGCTGTTTTCCAGTAGTATGACAGTGA
siSG1009 6	36	G C	---			GTGAGGAAGATGCTCTTCTCCCTCCCATGAC[C]/G[C]/GGCTTCCCGGGGACCTGTGCGTTTTCC ACCCGAGACGGCCTTTGTAGGGACCCACTGCCCACTCCGCTGTGCGCTGGGTCCGCTCTAG GGCTCGAGTGTTTAAAG
siSG1011 8	107	C A	---			TAGGCTTAAACCTGGAACTACAAAGCCAAAGTCCCTCCCTGGCTGAGGGCAGTACCCTCCATGGGC ACAGTCCAGACCCAAAGTCAAAGATGCCCATTCCTTGG[C]/A/CCTAGCCCTCAGTTCCTTCATTTCC ACCAGCCGTGCTGTTGAGTTTTCTCCCAAGTGA
siSG1012 0	89	T C	---			TAGTAGGTAAAGAAAGCAAGGAGGATGCTTATGCGATGACTGTTACAGTGGTGTGAGACTATGC CGTGTTCACGAACACTTAA[T]/C/GTGTGTGTAATCTGATTTATCCTCGTCTTACAAATG
siSG1017 8	42	C T	---			TTGAGCAATATTGTCTAGCACTCTGCTGGACATTAAGTCCG[C]/TGGGAGGAGAAGTGAACAGGAA TCGATTCTTTGTCTTTAACTGCOCTTAGTTAGGAGATGTTAAATACTTGGC

stSG1019 3	136 GA ---	---	---	GGAACAATACTACCTAAGGACAAAATACTATTATTAACAAAAAGTCTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTAC T[G/A]TTTGAAACTGAGATTTAAGTTGCAAACT
stSG1020 2c	143 GT ---	---	---	AAGCTAACTTAGGTGAATGGTCCCACTCAAAAGTCTTTCCGAGGGAAGCTCAGTCTCGCTTGGCGAG AGTCAGCCCTGGTCACTCATAACGGGCTCCAAGCTAAGCGTCAAGGAAGAGTCCCACTGCTTCT CGCTGTCA[G/T]CAAGACCACAAAGGCAGATGCCACTGCTGCTCTTCTTCTGCTACTTTCT
stSG1020 9b	75 AG ---	---	---	TCCTTTCTCTTTCACTCTCAGTCACCATGATTCAAATAAACTAAATCTCTCTTAAGATCCCACTTTAT TTTTA[G/C]TCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	---	TCCTTTCTCTTTCACTCTCAGTCACCATGATTC/TAATAAACTAAATCTCTCTTAAGATCCCACT TTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	---	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCIGA
stSG1025 2	108 AC ---	---	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAATAATGAGAAGATTCTTTATTTTGGACCAATTTT AGGCACTTAAGAGTTTCTTTCTCTCTTTCCCTTTGATCA[AVC]AGTGAAGATATGATAGGGAATTC AGAAATTCCTCTCTTG
EST10915 0	123 AC ---	---	---	CTGTATTAATTAAGAAAGGCACATTAAATGAGGGACGGAAAAATCTACCTGTACACAAAATTTCTGTAC TTTAACAGCATCTCAATAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG[AC]ATTTTAA GAACTGAGTTATTGGAC
EST11023 1	166 TA ---	---	---	TTTTTGTTAAACCAACCCCTGAAAGTTCCACATGTGAAATATAGATACAACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACAGTAAACAGCAGGGC AATTAGTCAATTAAAAAAATAGTACATGTTAT[AT]GTGTAATAAAATTTAAATTTACAAAGGCTTT TCCACTCGTGGATTGTATCTCTTTTGGAGGGAGGAGTAACTCTGG
EST14096 8	71 GC ---	---	---	GGGATGTATATTACAGATAACACAACCTCACAATAATACCATCAGACATTGAAAACATAAGGCCATTCT GTGA[G/C]TTATTTTAAACCTGGTGTTTGCACATAATGATCTTAAAAAAAATGAAATACCAAA ACCAAGATTCTCTCTTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 CA ---	---	---	TGCAATTGTGAGAAGCAGAGGGGCCAACCCCTGGACCTCATCTCTGTAGATGTGAGGTCG CAGGATGCTTAAGTCTCTCTCTGGCAGAGACCCGAGGTGCAGAGATGATCTTCTCA[AC]CCCTTC TCTCAGGGTCGTGGAG
EST22555 7	60 GA ---	---	---	TCAAGCATGTGTAAGGCACCTGCCCGCCAGACCCCTTCTAACTTCTGACACTGGAAGGTG/AJAA CCTGGGAGAGAGAAGACACTCCCTCCCTAGCTTCTACCTGGGACCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGGCTCAGAG

EST22917 6	74 C T ---			GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC[CT]TGACATGGGGCCAAAGACTTCCAGACAAAGCACGCGAAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---			CAAGTTAGAACCATGTCATCAGCTTTTCATCCATGGTGTAACTTAACCCCTCAGGCTGTCTACTCA[AV G]TGTTGGTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAGTCACTCTCCA GAGGGGGAACCTTCAAAGAGGATTCCAACAGTGAAGCAGAAATCATGGGCGAAAGTC[AVG]CTATGG GGCCAGACTGAGGTTGGACCAACAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
EST36745 3	56 A G ---			TGTGACCATACCAAAACCTATGCAATAAAGAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTGAAGTGTGAATAAAGTTTCATAGCAATTTTGGGA ATTATGGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG T[AT]TATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410c	201 A T ---			TGTGACCATACCAAAACCTATGCAATAAAGAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTGAAGTGTGAATAAAGTTTCATAGCAATTTTGGGA ATTAT[GT]GTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410b	139 G T ---			TGTGACCATACCAAAACCTATGCAATAAAGAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTGAAGTGTGAATAAAGTTTCATAGCAATTTT GGAATTTATGGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410a	48 C T ---			TATCGTGGGAAGTTCCAAACCTCATACTTATGCTGCTTTTCTACTTGCTAATATGGATGCTCTTGCCA GGCTC[CT]TTAAATTGTCTGTAACTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA
STS- R42778	74 C T ---			CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCCCTCCGGGATGGTGAATAATGTTCCGGACCTAGATA[CTG]TGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---			GAAATAAACTAAACTGCAAGCAATCACTGTTAATAAGAATTGTTCTTCTGTTT[CT]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGAGCAATGAGGCTCCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
siSG1026 6	55 T C ---			GTATAATTCAGCATAAGCCCAAGCCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTTACA AGAAT[G]AAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
siSG1028 2	70 T G ---			CACCTTTAGATATGAGGAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGATATGCAATAACAGCAATAATTTTTTCACT[CA]TTG TCAATGCCAATGCATTGAAAGGCCCCAGAAAATGAGAAAGGATAACAAACCTTTTGATAAAAAAGGTA AGAATTCTGTGTG
siSG1031 0	128 C A ---			

stSG1033	116 TC ---	---	TTTAAAGCTACATGCTCTGAAAGATGATGCTGCTGATTGAAATAAAGGAAGAAAGATGCATTTCCGG GCTCAACCTGTCTAGGAAGGCTAGACCTCAACACCAACACCTCCATCJGCAATTTCCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
1b			TTTAAAGCTACATGCTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGATGCATTTCCGG GCTCAACCTGTCTAGGAAGGCTAGACCTCAACACCAATJACCTCCATGCATTTCCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1033	107 AT ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAAATGGTTTTATAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGTAGCTTATGCTGCAATCCAGCACTTCGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGATTCGACACCCAGCCTGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTCG/AJAAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGCAGTTATTT TGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGTJGJTCATCATTAAGAA GACAAAGGGTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCGTGG TCGTCTCTTTCCAGTCTCTGCCAGAAAGCATCCCCATGATGTTGTGACCGCACAGCATTGTGTCT TJGJCTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATGTGTACTGTCTGCTGCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTTCCAGTTTGGCTTCTGTCTCTGCTCAJTCJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGCTCCTACTCCCA AAGTCCATAACTCAATCCTTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTCCJGJCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCTCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGJTCJTTTAATTCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCCCTTAGTCTGAGATGGGTA CACACCCACAAGTTTCATGTAAATGCCAAGTATCAACTCTTGAGGACAAGGCAAAACCAAGTGTGCA JGJGAATGTGGAGGATGCTGTGTGCAAGTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAAAGGAA AATGCTCTGA
1a			ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAAATGGTTTTATAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGTAGCTTATGCTGCAATCCAGCACTTCGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGATTCGACACCCAGCCTGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTCG/AJAAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGCAGTTATTT TGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGTJGJTCATCATTAAGAA GACAAAGGGTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCGTGG TCGTCTCTTTCCAGTCTCTGCCAGAAAGCATCCCCATGATGTTGTGACCGCACAGCATTGTGTCT TJGJCTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATGTGTACTGTCTGCTGCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTTCCAGTTTGGCTTCTGTCTCTGCTCAJTCJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGCTCCTACTCCCA AAGTCCATAACTCAATCCTTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTCCJGJCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCTCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGJTCJTTTAATTCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCCCTTAGTCTGAGATGGGTA CACACCCACAAGTTTCATGTAAATGCCAAGTATCAACTCTTGAGGACAAGGCAAAACCAAGTGTGCA JGJGAATGTGGAGGATGCTGTGTGCAAGTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAAAGGAA AATGCTCTGA
stSG1243	225 GA ---	---	TTTAAAAAAGAAATCTGTTCG/AJAAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGCAGTTATTT TGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGTJGJTCATCATTAAGAA GACAAAGGGTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCGTGG TCGTCTCTTTCCAGTCTCTGCCAGAAAGCATCCCCATGATGTTGTGACCGCACAGCATTGTGTCT TJGJCTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATGTGTACTGTCTGCTGCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTTCCAGTTTGGCTTCTGTCTCTGCTCAJTCJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGCTCCTACTCCCA AAGTCCATAACTCAATCCTTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTCCJGJCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCTCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGJTCJTTTAATTCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCCCTTAGTCTGAGATGGGTA CACACCCACAAGTTTCATGTAAATGCCAAGTATCAACTCTTGAGGACAAGGCAAAACCAAGTGTGCA JGJGAATGTGGAGGATGCTGTGTGCAAGTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAAAGGAA AATGCTCTGA
b			TTTAAAAAAGAAATCTGTTCG/AJAAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGCAGTTATTT TGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGTJGJTCATCATTAAGAA GACAAAGGGTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCGTGG TCGTCTCTTTCCAGTCTCTGCCAGAAAGCATCCCCATGATGTTGTGACCGCACAGCATTGTGTCT TJGJCTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATGTGTACTGTCTGCTGCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTTCCAGTTTGGCTTCTGTCTCTGCTCAJTCJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGCTCCTACTCCCA AAGTCCATAACTCAATCCTTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTCCJGJCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCTCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGJTCJTTTAATTCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCCCTTAGTCTGAGATGGGTA CACACCCACAAGTTTCATGTAAATGCCAAGTATCAACTCTTGAGGACAAGGCAAAACCAAGTGTGCA JGJGAATGTGGAGGATGCTGTGTGCAAGTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAAAGGAA AATGCTCTGA
stSG1345	60 GA ---	---	TTTAAAAAAGAAATCTGTTCG/AJAAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAACCTAGTTTGCCTTCTTACJG/AJCGCT TCACATTTTAGCATGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGCAGTTATTT TGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGTJGJTCATCATTAAGAA GACAAAGGGTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCGTGG TCGTCTCTTTCCAGTCTCTGCCAGAAAGCATCCCCATGATGTTGTGACCGCACAGCATTGTGTCT TJGJCTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATGTGTACTGTCTGCTGCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTTCCAGTTTGGCTTCTGTCTCTGCTCAJTCJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGCTCCTACTCCCA AAGTCCATAACTCAATCCTTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAG

stSG1847 b	95 G A ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAACTTGATCACTGTGCT TCAACACAACCTG
stSG1847 a	49 C A ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTAC[C/A]CTAAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCCTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAACTTGATCACTGTGC TTCAACACAACCTG
stSG1897 a	83 A G ---			CTTAATGCCCTTCTCTCTCTCTGACAGGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACTT[A/G]CCCCACCACCTTCTCTCCGGTCTCCCAAGATGACT
stSG2022 a	86 T C ---			TGCTTGAGGTTTCAAACTGAGATATCTATGGCAAGTTTATAAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATACAT[C/J]ATTCATAATCTCATCTATTTAACATTAAACACAGGCCTTTGTGTG TGTTATTTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGCCCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---			AAACGTTGTCCCAAAATTTGTTTCAGTTTCAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTGACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71 A G ---			TTGAGCAACAATGATTGCGAATTGGGCAGCTCCAAACCAAAAAATGATT[C/G]AGGGGCTCCACAG GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---			TTGAGCAACAATGATTGCGAATTGGGCAGCTCCAAACCAAAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---			TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTCTATTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCCTGGCATGGCGATGGTGCAGGTGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAG[A/G]AAGTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTGTTTGTCTG
stSG2141 a	113 C T ---			TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTCTATTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCCTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAGTTCCCTATTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTGTTTGTCTG

stSG2148	50 A G ---	---	TGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTTC[A/G]AAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGGTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT [C/T]GCCGCGTACTCAGCTAATGCTACCGGGTGGAGCGCACACCGAGCCGACCCCTTTTCCAT ACCTGGCAGAGGAAAGGAGTGGAGGACCA
stSG2189	41 C T ---	---	CAAGTGGTGAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACCTCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/C]TTTATATTATGTAT AATGCTTACCTGATGATACCCAACTATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTCTGCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAACTCTGTGAGGAGGCTATCAGAAAGGGCAG[A/ C]GTCTCAGGAACTCTGCCAAGCACTGGGCTGTCTCCTCAGGCAGAAATTTCTCCT
stSG2306	67 A G ---	---	GTCATCAGCGTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCCTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGAGGGGCTGTGGAGGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAAATGGTGAATCAACAAGACCTCAATTTGCTTGACTGCAGAAGTAAGTGTGTCAC[T/C] GTTCTCAGAGTCAACATTACGGTGACTGTGTCTATTTCTGGCTGTCTTCTTATCA
stSG2465	76 C T ---	---	CAAGACTAAGAAGCCGCCACCCGAGTGGTCCACTCAAAAAAGAGATTTCTGATTTCTACCTCAAATG CAGAAACCA[C/T]TACAGATTAAAAAGAGAAACACACACACACTTTTGAGAAACTGCCCCCTTCCTC ATCTTCAAAGTGGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTGTATTCACAAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTGATGACTGGGTTAAATATGCAAAGCAGCTAAAG GAATATT[C/T]ACACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGGAAAATTCAGAGGATTTTAGACCAACTTTGCCCTGTTCATTCCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAGCA[T/G]GAACAATC CCGGCCCCAGATTAATTAT

stSG2577 a	121 C T	AATTGCCAAATGGAATATCCAGAGGATTTTAGACCAACTTTGCCCTGTGGCATTCGCCAGTTTGGT CCCAATATAGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[G/T]ATGAACAATC CCGGCCAGATTAATTAAT
stSG2700	58 G A	ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTAATTAATGAAGTCTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGGCGGAAATAAACCACTGGTCCAGAGCAGAGGAGGCTACTTGAGCCGGACACCA
stSG2724 b	101 T G	AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTGCTTTTATTAATTAATTTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGCATAATCA[T/G]TTTTTTTAATCCTGGGGTGTGAAAGAAC
stSG2776 a	65 G A	GTGGCGATCTTTACTTTCCAGAAAGGCGGTAAATAAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATTGGCCCTTTTGAGTTAGGCCAGGAACCTTCAACAAGGGACACTGCTGGCCAACCCACAAA ATATCCACTAATCCCGAATATAGTAACCTGCTTGTCGGAATG
stSG2791 b	109 G T	AAGGAAAGGTGGAGGGAAGGAAGGAATTAACAATGTTAGAAAGAGCAACTAAAGATTATTTTC TATTATACCTCTGAACGGTAAACTAGCAATTTTAATAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2791 a	100 A G	AAGGAAAGGTGGAGGGAAGGAAGGAATTAACAATGTTAGAAAGAGCAACTAAAGATTATTTTC TATTATACCTCTGAACGGTAAACTAGCAATTTTAATAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
			CCGCAATTTCAACACACATTTCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAACAA[C/T]GAACAAAAATAAAGAAAAAACCCTATGAAATGCCCAGGTTTA ATTTTTTTCC
stSG2826	85 C T	ATGGGTGCATTGTAAAGGCAATTAATACTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
stSG2850	88 G A	ATACTCACGGGGGCTGAAGGGCAATGTGAAGAGTGACTGCAAGTCTCTGGCAATTTCTGTGGTGCAGC AAAT[T/C]GCCCCCTTTATTTAATGATCCAGACATCTGGGCAGCATAGCT
stSG3031	71 T C	GTCCCAACTCCTCCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGGCCAAAAGGCAAAACTGGCTGAGGC
stSG3058	81 G A	CAGCATCTCCAGAACATCTAGAACTGAACCATCTTGTCACTATTGAAAAACAAAGCCAAAGTTC CAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATCTTCTTATGGTTCAGCCCCCTACTTT AGTT
stSG3092	94 T G	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTAGTCAATTTGTCAGTGGAGTC[A/G]TGGGGTGTCTAAGTGTCTGAACTGAAGTAG
stSG3230	95 A G	ACATCTCATCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGOC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTACCAACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGT[G/C]TGTACTTGGCTAAGTACTTCATGCTTAT
stSG3245	160 G C	

stSG3265	42 T C ---	---	AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAAT/CJGCAATGTGAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTTTCAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTCACTACAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTTTGTGAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141 C T ---	---	TGTACTTACTGTGTCATCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TJGTAGATCCCCAAGTCCCTGACACATTTTCTTAAGAACT
stSG3269 a	24 A G ---	---	TGTACTTACTGTGTCATCTATCC/CJG/TJCCCTTCCCTGAGCCTGGACTGCTCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3284	130 C T ---	---	TTAACTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAATGACTAAATTACAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA/C/TJ TCCCTAACCTTTGTTAATTGCTGTAATGGGACATTTGTTGTTTGATCTACCC
stSG3292	99 A T ---	---	GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATGGACAAGTGACTTAAATATCTAA/JTJACAAATCAATAGCATTTTCTTAACITCAA
stSG3323	26 C A ---	---	TAAATGTCATATCTTTAGCTCTCACT/CJ/CAGTGTATCCATTTCCCGAGCGTAGAGCTTTCTG TTCTGTAGATTTGCCTGTCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCTGAGTGTCTTCACTTCTTTAA
stSG3369	69 C T ---	---	GATCCCCAGTATTATTTCTAAATTTGAACCTTGTTTGTGGAATAAAAAATCTGAGGACCCTCAGAG GG/C/TJATAAGGGAAACCTCTTTGTCTTAGTTCATAAGGACTTTCT
stSG3398	125 G T ---	---	CAAGACTGTAAGAACGTAGGCCCTTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCGAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACTTTGTAGC/CJ/TJCTGGGT CAAAGTCTAAGAGGACAAATAAATAGAGACT
stSG3416 a	43 A G ---	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG/CJ/CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCTCTCCACTCAGCCAACTGAGTAGCTGGCTGCAGGACAAAGTCAACATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3424	173 T A ---	---	GTAAGACAAGGTTTTGCTATGTTGACCAGGCTGGCTTGAACTCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCGCCGACCTTTTAAACTGAAT GTTGAAATCATCTGCTCTTGTCTGGTAACTGAT/JCAAGTTGCTTAACCTTTGTGAAACCAC TTTCTTATCTGTAACAAAATGGACAAACAGAACTTTTCTTCTCTCTC
stSG3436	88 T A ---	---	GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTCAAGGTGATGTGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGGCCCTT/A/GAAATAGCTTACTCTGTGTTTCTTATC

siSG3463	103 C T ---	---	GATACAGAAGATAGTGGTATGGATGGATAGTAGTGAAGGACAAATAATACAAATATATTTATTG AAATAACAAAAATGCATACACAGCTCAATGGGTAC[C/T]TGGAAACAACTTGCTTGACTATATTA CTGA
siSG3491 b	71 G A ---	---	CAAGATACTTCATTGTCTAAGTAGTGCAGTGTGGCAAAATATTTCTCAGGAACAAGGACGATTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTACTGGCACCTGTGGATTCTATTAACACTCAATTTACTATTTCTGTGATG ACAGAAAAATAAGTTAAC
siSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTT[A/C]TGCAATATATGTGTACAAACACACACACACC CCTAATCTCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
siSG3536	213 A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCATTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAG[A/G]TCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
siSG3583	112 G A ---	---	GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
siSG3586 a	60 G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGT[G/C]ACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGGACTGCTTGAAACCCAGGAGTGAGGCTACAGT GAGTTATGATGGCGCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
siSG3589	101 T C ---	---	ATATAGTGTGGTAGCATTATAAATCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCACCCCTGGCACAAAAACCCCAATGAT[C/C]CTATTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAACAAAAAGCTATATACAC
siSG3590 a	70 A T ---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AA[A/T]TTCTCTGATGCTCTTGACCCCTGTAGGAAACACATTTCAGTTTCTACACT
siSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTTA/CJAACAACTCCAGAGAAAACTGGGCTCTATATATTTAAG
siSG3644	40 T C ---	---	ACATATGTAAGTCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GATTGAGAGGCATGAACCAAGG ATCGGTAATAATCATTTATGAAATAATAAGTTATCTGGGGAACGGCCATTGTGCCAACATTTACTAA GTGCTCTACTA
siSG3646 c	70 G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATGATGATAACAATAATATGCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

siSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAA/GIATGTCTT ACTGGTGATATAACTTTGATACTTGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG/A/TTGATAACAATAATATGTCTT ACTGGTGATATAACTTTGATACTTGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85 A C ---			ATTGTTTCCCTGAACATCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCCTACGAGGC/A/CTCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
siSG3693 a	30 C T ---			ATTGTTTCCCTGAACATCCCGTGGTCTCC/C/TCTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
siSG3698 b	145 G A ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATGGCAGAGGAGCTCCAGGAAATCCACAGTTCTTGGAAAGAGAGGGGCTCTAAGTCT TTATTGGG/G/AJAGAATACCCACCCACCTTCCCTCACTGCAGA
siSG3698 a	51 C G ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGTTG/C/GTCTCTGACTTCCA CCATTCACTGACTTTATTTGCCAGAGGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATAACCCACCCACCTTCCCTCACTGCAGA
siSG3724	107 C T ---			ACGAGCTCATGTGCAGAGGTTCTCTGCTGGATCCCACTGGAGCCATCCCTGGGCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGTGTAAG/C/TACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
siSG3725	104 G A ---			GCCAAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATACAGCCCAACAGCAACAGCCCC/G/AJAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
siSG3751	128 G A ---			CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGTTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A/T] GCTGACTCCATGTGTTGCAAGAG
siSG3787	49 T A ---			TTCTGTGCAAAAGAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTA/T/AJAAAGTTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAATAAGGAGTGTAGGCTAAAGCAGTATCTTCCCCT
siSG3880 b	115 G C ---			GACAAGAGGGAAGAGATGGGCCAGAGACAGGGCTGGGGCAGCTGGGGTCCCTGAGTGGCCAGGGGC CACCACAGTCTGTGGGTCAAGGCCCTCTCTGGGGAGCAGGTCTA/G/CJGGCACGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCCT

stSG3880	a	36	G C ---	---	GACAAGAGGGAAGAGATGCGCCAGAGACAGGGCTG[G/C]GGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACAGCTCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGTCTAGGCCACGGAGGATGCAG GGCTGGAGGGGACCCCACTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT
stSG3895		44	A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[A/G]JTJTJTJTJTJTJTJTJTJTJT TACATGCCCTCATAGATATATTCAATTAGTGTATATCACCATTGGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902		104	T C ---	---	TCGTGTGAGACTGGAGAGACCAGGTACCAAGCACCCAGCTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCACTAAATGTGAACCTGCTTTCTTTTC[C/C]CAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935		50	G A ---	---	GGGTGTGTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
stSG40		25	A G ---	---	GAGGAAGAGGTTGAAGAAAGTGTGA[A/G]JAAATATATTAAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCAA
stSG4009		32	A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCTC[A/G]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATTCCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCCACACTGCTTACA
stSG4033		123	T C ---	---	AGAAAGCCTTGGGACAATGGCAGTGGCCCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT[C/C]JGTGAAC AGGTGGGCAACAC
stSG4038	a	29	G A ---	---	GCTGAGACAGGTGTACAGCCACGCCCTGT[G/A]CGGAGGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCAOCTGAGGGTTCATCACT
stSG406		53	T C ---	---	ACTGTGTTCAACAGTATTGCGTTGTCAAGACTAGGAAAGCTAAACGAACAAA[A/C]JGGTTTTAGTT TTGCTGAAGACTGGCCCTTATTAATGGACAGCTTTCCTAACAAAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095	b	55	G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTTAGT[G/T]ATAAAAA GTTTGCTTCTGTAATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095	a	27	A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGT[C/A/C]GATACTATTGTCTGCTAGATGTTATAGGATAAAAA GTTTGCTTCTGTAATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120		65	G A ---	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G/ A]CTTTTCCCCTCAGAGAGCCCCACAGTTAAACACGTTTCCAGCACACCATTAATCCACCGAGCT

siSG4128	54 A G ---				CTTGGCAGATAAGGACTCGTTTGGAGATATGACTTTCCTTTGTGTACATTTCTT/GJGTATATATTT TACTTCTTCTGAAATGCCACATAATTTGCAATAATGATTCACTCTTAGCTCCCAAGCAAGTCC TTTATCAAATGCAAATGTTCCAGAGG
siSG4209 b	128 G A ---				CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGCCGCACTCCCTC[G/A]GC AGGGGACCAACGAGGCGACAGGTCTTGTATGCTCCGAGAGCTGAGCTCCATTCCA
siSG4209 a	65 G A ---				CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /A/CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGCCGCACTCCCTCGGC AGGGGACCAACGAGGCGACAGGTCTTGTATGCTCCGAGAGCTGAGCTCCATTCCA
siSG4254 b	31 G A ---				CATTACCCAGAACGCCATGGAGGACCAAGC[G/A]CCACGGCCGGGACTCCCGGATGGCTGGGGG GCTATGGCTCTGACAAGAGATGAGCGAGGGCCGGGGCTGCTCTCTCCAGGGGAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTGATG
siSG4301	81 T G ---				TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGGTAGTGGCTCCACACTTTCAT TTAAGCAAATAAATTT/GJAGCTTCTGAGTAGTTGTTCCAGTTTCACCCCAACATTTTG
siSG4331 b	71 T G ---				CTCACAAGGGCCACACAGAAAAGATACAAATACATTCATCCAGCTAATATTTAGTTTTATGACAC AGAGT/GJTTTTCAACAAGTTTAAAGTGCACCTGAAGAGCATGTTAAAAAGTTTAAAGTTATCACTT GGAGACGAGATTTCTGGCCCTCGCCCTTGATTTGTTGAGGGGTGTC
siSG4340	76 G A ---				TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGGAGATAACAATGTTGATACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---				TTCCCAACCATTGAGTGACAGAGCTCAGTCAATGCAGAACTCAGGTTTGCATGACTCAAATTAGG AAGTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTGCACCTTCACAACCTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
siSG4361 a	24 T C ---				TTCCCAACCATTGAGTGACAGAGCTC/CJAGTCAATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTGCACCTTCACAACCTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
siSG4376	73 A G ---				TTTCACTGCTACTGGTTTGGGTCTGAGTCCCTCAAACTCTGCTTTCGAAGTGTCTTCCAAAGGGGAG AACAG/GJCTGGAACCTCGGCTCTGCAAGAGCCATCTTCCAAAGCCATTTCTTCTCAGCTGC
siSG4381	50 T C ---				GAAAGCCACAACACTCCATAGCCAGAGAATGACAACATACGATTTTCTTTT/CJTCAGTCTTGTAGT ATCCACAGTAGTGTCTGTCCATGTACAAAGTGTCTGCCAGAACACCCCATTAATTCATGCC
siSG4410	79 A G ---				ACCAATGGTCTGCTATGTGATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAAACCCCGC/GJTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65	C T	---			AGCAGATCAGTCAGCCACATTGTCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430	54	A G	---			TGTATGCAATGAGAAAAATAACCAACTGTTAGGATGGGGAGGGGAGGAGGCAATAGGCAC
a						AAATGGAATCTATCTCTGGCTGCTCTCTCAGGTC
stSG4448	99	G A	---			ATGCACATTAAATGAATGGCCTAACTACTGGGAACCTTTAGTAGTTCTATAAGGT[A/G]ATTAAACATA
						GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATT
stSG4449	92	T C	---			CTCCCTTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCTCCCTCCCTCCCTCCCT
						CGCTAGCCCTGCCCCTCTGGGGTCACTGC[G/AT]GGGTAGGCCCCCAAAAA
						ATTAGCCATTTCATCTTGAACAAATGCTTTACTGTAAGAGTACTGTACTGATGATGTTTACAAT
						TAACTTTGGACAACCTTAAACCTTA[T/C]TAGTGACATTGCTGCTAATAATCAAAATACATTCATCATA
						GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCG
stSG4467	42	C A	---			CAGACATGAGGGATGGCCCTGTCTCTCTGGACAGAGCCCTCA/C/AJAGATGATGTCATGTTTGTGT
						GAATGAAACTCAACACTCTCTCAGTTTTTAGAGTCATTTCTGGTATCGAGCGCACACCGAGGAG
						CACACCTGCTTCCAAAGGCTGCTGCCCTCTGCAACACAGT
stSG4475	21	A C	---			ACATGTCAATTCCTGACCAGG[A/C]TATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAAACTGGACTTTTGTCTTTTCTTTACTGTAGACCCAGGTTTCATG
						GTAACATTCTGGGGTGGGGTGAGACAAAC[A/G]ATGAACCAATAATTAATTACAATTATACATT
						TCAAGGAGACTTTTAACTAGGTTAATGTGAACGAGCCATCAATGTTTGTGAGGAAAGGGAGA
stSG4477	32	A G	---			TGAAGTCTGCTGCGGCAACGTTTGGCCTCATTCAGTCAGACATGGC
						TGAATCAGAGCTGGTGGGAGCTGCAGGAGGGGAGGCTGGGGCCAGATGAGCCCGGGGA
						CAGCAGGCGTC[G/TC]CCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTTGGACTCGATCT
stSG4531	79	C T	---			GATTCTCATTGACAGGGGAGACGCTGTTGTCATCAA
stSG4550	86	G A	---			TGCATTAAAGGAATGATACGGCATATTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
b						AAAAGAGACAGTGGCAC[C/G]CAATTGGAGGGGAAGGCGGGGAGGCTTTTAGAGAAC
stSG4550	85	C G	---			TGCATTAAAGGAATGATACGGCATATTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a						AAAAGAGACAGTGGCAC[C/G]GCAATTGGAGGGGAAGGCGGGGAGGCTTTTAGAGAAC
stSG4590	47	A G	---			AATCAGGCACAAGCTCGGGAGAGAACCAAAAGCTCTTCTGCAC[A/G]ATGGAGGGAGACAC
						CATTGAAAAGGCATCGTTCCTTCTTCATGCAAGCGAGGCTGGCTCCACAGGATGGTCTCCTTG
						AATCTGTATCACCAGCGTGGT[C/C]CAATGTACTAGTAGCTTCCACAGGGATTTTTTATACTATTC
stSG4623	22	T C	---			CTATAAGGTTTTATCATGAATAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTTCACATTTATCT
						TAATATTCTGTTCAAGATGCTCTGGAG
						TAAAAAAAACACCCCCCCCCAAAAACACCCAGAGTTTTTGAGTTTTTATGTTTTTTCAGATTTTAAAG
						GTAATTTCTTTCTTAGCTTCTAAATTTTGGATCAT[A/C]ATCAGAAAGTCTTCCCTACTCCAAGGTGA
stSG4843	102	A C	---			GAAAGGA

stSG4850 a	38	CT	---	---	GGAACTCTAACTGGGAATGCCGAGGAGGAAGGGGCTC/TGTGACCTTGACGGCCACGTCAGGAG AGCCAGCGGTGCTGTCGGGGAGGTTCCAAAGGTGCTCCGTGAAGAGCATGGCAAGTTGTCTGACAC TTGGTGGATTCTGGGTCCC
stSG4879	86	AG	---	---	AACTCTGAAGGGGTGACCTCAACCAGCCCTGTTCTGTGAGGTCTCTTTTGCAGAATGGCCTG CCCTGGGACTGGAGCAG/G/GCTTGGTGAGCTCTAGGTGGAGGGTGGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104	GA	---	---	ACTGGACTGGCTGCTTGCTGAGCCGGCTGAGCGCGGTGGGACTGCGGCTGACCACTGCTCTTCAG AGACTCGCCCGCGGTGACCAAGACTACGCTCTGCC/G/GTGGGAAAGCAGAAGCAGGACC
stSG4896	112	CT	---	---	AAACAAATCAAAACCAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA GGTGGGGGCGAGCTGAGGAGTGGTGGGGGCTGGGCACCTTTCTCTGAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22	GA	---	---	ACAGTGCCGATGGTTACACAAT/G/ATTGTAATGTATTTAATCCCACCTTACGAATGATTAATAATGA TAAATCTTATGTTTATTTTCATCACTACCAAAAGGCTGGGTGACGGGTGCTGGTTCTGGTCT
stSG4950	24	AG	---	---	TCATGACTCCCAGGAAAGTCTT/GTCTTAGCTTCTCTCCCTCCCTACTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136	GA	---	---	AGATACGGGCAAAACACTGGGATGGCTTCTTGACAACTTAAGAGGTCTCCGAGTTATTTCTGGGTT GGGAAACACTGACCCAGCCCTTATCCCTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC/G/GTGCACACAGATGGGGGCTGCTCTATATTCAAC
stSG4961	91	CT	---	---	GAAAGTCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGT/GT/GAGAGGGGCTTACAGGCCAAGTCAGCAACACAGACAA
stSG4967	72	AG	---	---	ACTGGTCCCTCTCAGCAGATTCAGGGTCTGTCAGGGGCTGGTACCACAACTCAGTAGGAGTGCAA GGGCT/G/GTACCCCGGAGCTAGACAGCCTGGGTTGAATCTCAACTTCTCCCTTTCTTGTGTGC AACCTTG
stSG4997	22	TC	---	---	CAAAGGAGAGTAGGAGCCCAAT/G/CTTTTAAATGGTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGATGGTGATCCAAAT
stSG6312	37	CT	---	---	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAAC/G/TTATGCCATGCGGGAATAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107	GA	---	---	GCTCTGGTCAAGCAAAATCTCCAGGACAGAAGCAACAGGACAGTAACACACATGTATGACCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC/G/GATAGTTTCAAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAACATTTTGTCTTTTGGCCTGGTGTGGACAGAAAGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

stSG6362	88 G C ---	---	TGTGAATGTACACTCAGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA/GCJAGAAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62 G T ---	---	CACATCTGTGTTTCTGGAGCAAGGGAAACCACAGAAAGGCAGGAGTTTGGGTGTGCACCTGG[G/T] GTCITTCAACTGGGTGGAAACCAAACTGAGTCCTTGAAGTCTCGCTCTGAGGCTGCAGAAAGATAGA TGGCTT
stSG8022	53 G A ---	---	AGCTCTGACTCCCTGTTGACGTGACGTGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAACTGGAAACTCTACAAATCAATCGGTTATTTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGATCTCC
stSG8032	67 G C ---	---	TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTACTTCCAAAGAATTCAGAAAAATTGTGTGTT G/CJTGGGAGGCAGGGTAGCAAGATAAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46 C A ---	---	AGCTGGCTCTTCCCTCTGTGCGTTCGGGAGGCTTACGTCCTCGCCCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAATTCCTGTACATCAAAACAGGGAACA
stSG8064 a	23 G C ---	---	AGCTGGCTCTTCCCTCTGTGCGTTCGGGAGGCTTACGTCCTCGCCCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAATTCCTGTACATCAAAACAGGGAACA
stSG8072	59 A G ---	---	CACATCATCATCGAGTAGGTGAGGACGAGGAGGGGTGGTCTTGTCTTAGGG[G/A]GTGGC AGAGGAGAAGGAAGTCCGAGTATTAGTGGCCGCGATGCAGTTCAAGCCTGTGCTGTTCAAAA
stSG8100	40 A G ---	---	ATACACCCACACACCCCACTCAACCTTGTATCAAAATTCATCAAGTGAACATAAGTATAAGAAAT ATCATGACTAGTTAAAGATAGCAATACCAATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138 T C ---	---	AAGGCTCCTTTGAAAGCATGGTTTATTGTTCCATTAACTTGTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTGCAATATTTGAGATGTACAGTGTGATGATACATGTATGTATACAATGTGAAA TGAT/CJTGTCAATAATCAATAATGGTATATTGGTTTAGGAAATGTGATGGT
stSG8105	110 A G ---	---	CAGTGGTTCTAACTCCAGGTACACGAGGATGGTCTTGTGCTTGTAAATACACAGATGACTAGGCC CACCTGCGGAGTTCCTGTTGGAGTCTAGGCCTGAGAAATTC[G/J]TTCTAACAAAGTTCCCAAGTGA CCCTGAGGCTCTTGGACTGGGGAACATGCTTTGAG
stSG8130 b	96 T C ---	---	GTGTGTACATCATTTGGGAATGGAGGAAATAAATGACTGGTGGTGGCTTTTAAAGTTCAAATTT GACATTCAGACAAGCGGTGCGCTGAGCCT/CJGTGCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36 C G ---	---	GTGTGTACATCATTTGGGAATGGAGGAAATAAATGA/CJGTGGATGGTGGCTGCTTTTAAAGTTCA AATTGACATTCACAGACAAGCGGTGCGCTGAGCCTGTGCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124 T A ---	---	TTGTGGACTTCAAATCTTTCCTTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAATTTGTGAACACAAATTAAGAAATGAATGAGATGTTT/AJCTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCTCTGTCTGTGAAAG

[illegible]

ESTD- AT3a	--	--	--	---	---	AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGAGGAATTTGAAAGGGCATTG GAATTCAGAGCAAAAGAGACAGATATTAAAGAGCTGGGGAATGTGG
ESTD- B3AR	--	--	--	---	---	GGCTGCCAGGGTTCCGTGGGAGGCGGCTAGCCGGGGCTCTGGGCGTGGGCTGCTGGCCACC GTGGAGGCAACCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAGACTCCAGACCATGACCAACGTT GTTCTGACTTCGCTGGCCGAGCGGACCTGGTGATGGGACTCTGGTGGTCCCGCGGGGCCACCTTT GGCGC
ESTD- BA511	--	--	--	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTCCACTGCA
ESTD- BCL2	--	--	--	---	---	AGCTGGATTATACTCTCTCTCTGGGGGCGGTGGGGTGGGAGCTGGGCGAGAGGTGCGGTT GGCCCCGCTTCTCTCTGGGAAGGATGGCGACGCTGGGAGAACAGGGTAGACAAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCAGAGGGGCTACGAGTGGGATGCGGGAGATGTGG GGCGCGCGCCCCGGGGGCGCCCCGACCGGGCATCTTCTCTCTCCCA
ESTD-BCL	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGGAGACTCATCTGCGCAAGA GACCAAGAGGTGAGCTTCTGTCTCCGGGAAAGGAGGAGGTGACAAAGTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCGCTGGCACA
ESTD- BRCA1a	--	--	--	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	---	---	ACTAAATGTAGAAAAATCTGCTAGAGGAAACTTTGAGGAACATTTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTGCTGAAATGACATTAAAGGAAAGTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGCTAGCCCTTTACCCCATACACATTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAGAGAACCTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCTAAATTTGCTCCGGGAAGCACATTTCATCAA CCAGTCAAGTTGGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCCTTCAACCATGCATTCCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	

ESTD-C7	--	--	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAATCAATAATGGCAATAGGAGAGACATCACCTGGGAATGTTAG GCAGTGCTTAAGTGGGATGGACAGACAAATGGCGATGCCAAGCCATAGGGGATACAAAGAC AGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGAACCCAAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCAATTATGGTCTTTCCGGGCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCGGCTTCTCTCACACATACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCATACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAA
ESTD-CB24	--	--	--	--	---	---	---	ACCAGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGTGGCTGTGTTTGAAGCATCAGAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACACAGTGGAGCTGAGCTGGTGGTGAATGG GAAGAGGTGCACAGTGGGTGACACAGACACCCGACGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	---	GTTTTCTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTGGCCGTG TCTGCTCTCGAACCCAGGCGATGGAGATCCAGGACACAGGCGTGAGGGAGGCGAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTGTCAACAGAGTCTTACCAGCAAGGGGTCTGTCTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCGGTG
ESTD-CB27	--	--	--	--	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTAGGTAAGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTTGCTATTCAGGAGTCTGTGGAGTCTGCTCATCAGCTATCTTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCTGCT TTCTCTGTTTCATCTGATGGAAGTCTTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTCTGTCACCTTTCAGGGTGTTCAGGTGGAAAGGT GAACAGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACATACTGCCTTTG GTCAGCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGGGACCTGGAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATATTTTATTTGACCAAACTATCATATGGAACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	---	GCCGCAATGCCCGGGAGTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGTATGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACTTCTCTCATCATGAAGAC TGGGAGGCCGGGCATAGTCTCATGCTGTATCCAGCATTTTGAGAGGCTGAGGCGGGTGGATCAC TTGAGGTGAGGAGTTGAGACCAACCTGGCCAACT

[illegible]

ESTD- D7S399	..	--	---	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTTCACAAACATTTTCATCCATGGACTCCATACCTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	---	---	---	---	GTGGGACACCGAGGCTCCAGGCTGGGCGCTTGCACGTGTGGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGTGGGCGCTGGACCTCACTGTCCCTGGGAGAGGAGGAGGTGGGAGGAGACA GAATGCTGATTATCTGTGGAGAACAGAACTTCTGGGCTGTGGGTAGGGGAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	--	--	---	---	---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGCGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	---	---	---	---	TCTGCTTTGTGCAGGAGGCTGCCGCGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCCACCGAGAGACCGGTACAGCCCCATCCACCCAGCCACCACTGACTCTCCCGACCCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCCGCCAAACCCAGAGAAATGGGCATGCCAAAG ACACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	---	---	---	---	AAGACGATGGCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCCCAGGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERBB2	--	--	---	---	---	---	TCTTTAGGATCCGCATCTCGGCTGTTGGGCATCGCTCCGCTAGGTGTACGCGGCTCCACAGCTGG GGTGAGGGGGTGTGGGTGAGTCCCGGGGGCGGTGCAGACCCACCGGGCTGGGAGGACTTCAACC CGCCTCACCTCCGTTCTCGCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	--	--	---	---	---	---	ACTCACAGTGTCTTTAAGTGAATGGTCGAGAAAGAGGACCCAGGAAGCCGTCCTGGGCGCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTTGGATCTCAAGGAGCGAGCATGTGCTGGACACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGCACCCAGGAACGCAATGCAAAACTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTCATTTCAAGAGTTAGTTTG
ESTD-F2	--	--	---	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCTCCAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGGCG AGCCAGTCCCGCGCGTGGCTGGTCCCAACAGAGGAGGCGCGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	---	---	---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTAAAGTATGATGTTTAAAGTCAAACTTCATTTTTTTTTTCCATA GGTATGTCCAAATTTATCCAGGACAAATTTGTTAAACAAAAAAC

ESTD- GODH	--	--	---	---	CGCAGACCGGTGAGTGTGGGTGCGGAGTGTGGAGGAAAGGAGGAGGAAGTGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGACCTCTGTGTCGACCGTGTGTTCTGCTGCCCTGTTAGCTGTCTGTGCTGCGCAGTCTGA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	--	--	---	---	GTTTTATGCATGGCAGCTTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGCTGG AGCAGGAATGCCGAGCGGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCAGGTCACAG
ESTD- GNAT2	--	--	---	---	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCACAGGCATATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCTAGG
ESTD- GPPK2L	--	--	---	---	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	---	---	CTGGGCTCGCCCGCAGCAGCTGCTGGCACCTGGACGGCGGCGCCAGGCTCACTCTATAGTGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	---	---	TTGGAAGTTCTCCACTGTTAOCAGTCTATGTTGGCAATGTGGCCTGGGCCACATTCCTGGCCTTG AGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTCTACTATATCTCAGATGACA CGCTCACCAAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTCTTTATCCCTGATGATGGATTGGCTTCTCTGCTG
ESTD-HT2	--	--	---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTTACAGTTTGTGACAGAGAAATAAAAGATAACCTGGGTTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAAACAAGACACACCTT
ESTD-HT4	--	--	---	---	ACCAACGAGCCCGGATACAGACACTCTTAAGTTTGCCTAAGGCTCATTCAATCATTAGGCATTTT CTGATAAACTAGGTTCTGGTGCTTCTATCGGCAAGAATGCGTACTATTGTAATAGTAGGTTAA ACCACAGCCCGCAAGAGTCACTGAGACTGGCAGCTCTGCAGCAGGCGTGAACCCCGTAGCCCTAAA TGACAGCCGAAGAGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	---	---	AACACAAAGCCCGCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTTCTTCCCTTCATCTTATAGATTGATGTTATGCTCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCCTTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	---	---	ACCCAGTGGAGCCCGCTCATTGACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGGAAGATGTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	---	---	---	TTTACTATTTCAATGGATACAGAAATGTGGAGTCACTATATCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	---	---	---	CAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATATTATTATTATTTTATTTT AGATGGAGTCTGGCTCTGCACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCCTCGGGTTCATGCCATCTCCTGCCCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTGTGCAATTGCAGG
ESTD- KRT10	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCATTTAAAGTAACCTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGTAACCGTAGCAAACTGCATTGGTATTAGA AAAATAAAAATTTCCAATATGTAGTGTGTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCGAGGGCTTCCCTTACCCACAGA
ESTD- LMP2	--	--	---	---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTTGTAGGAATGGAGTTGA CCTTCCCAAGGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	---	---	---	TGTCAGTGTCCCTAGGGGCACTCAACACTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGTTTTGCTTAATTCATCAATGCTCTTCAATCTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATTAATAATTTTTCACCTG
ESTD-MCC	--	--	---	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCCAAGCTCTGTCCCTAGCCGAACCTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTTCCAAGGGTTTGGTCTAAGTTGCTGATTACCCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCCCTGTTTAGCATGG
ESTD-NF1	--	--	---	---	---	ATTATCCAGATGAATTTACAAAACATATACCAGATCCCACAGACTGATATGGCTGGT

ESTD-RDS	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAAGAGCGTGCCGGAGACCTTGAAGG CCTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACAGGTGGAAGCGAGGGCGCAGACGCAGG CCAGGCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAT CCAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	CTTGTGACGGGAGGTACGTCTCCGCTCTTTTCATGGACATATGGATGAGTGTGACCATTTCCC CTGCTGACAGTGTATGACAGCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTCACACTCATGCCCC TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTCTGTGAACCCCCAACCCCTGCCTCC CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	TGAAACACCCCTGTGGTCCGGAGCCAGGTGTGTTCTCCTGGGAGCCTGAGGAGTTGTGTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCCTGGACATACACCTTCACTTCCCTTTGGCCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCTGGCCTGTTGTGCACACCCCTCTGTGAACCCCCAACCCCTGCCTCC CCACCCCAAGCCAGTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	TTTCACTTTGTGGATTGTTCTTTTGTGTGCGAGCACCTTTTCAACATGATGTGATCCCATTTGTCTCAAG TTTGTCTTTGGCTGGCTGTGCTGTGGGATATTTGAAAGAGATCTTTGCCAGTCCCAATGTCTAGAGAG TTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGGGCTTAGATTTAAGTCTTTAATCCATTTTG ATTGATTCTGTA
ESTD-IAT	--	--	--	---	---	AAATGGTCAGGACCCTGATCCACAAGAAGTGGTACCATTTTCAGGGCCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATCTTAAATGACTTGTGGACAGGATCA ATTCTCTCACCCTAGAACGTTGTTTACAACCTTTCTCCAGTATGGATGGGATTATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACATCA
ESTD- THPB	--	--	--	---	---	TGCGGCTTCTCCTCGGCGAGGTAGACTTCTTACTTGGCTGTGATTCCAAAGAGAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCATTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGAGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCCCTCAGAAATCGAGCAGGAGGATGGGAGTGGGGGTATCCTTGTATGCTT GTGTGCCCAACTTCCAAATCCCCCGCCCGGATGG
ESTD-TYR	--	--	--	---	---	TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATCTCTCCAGATTTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATTGATGTCTCGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

ESTD- TYRP1	--	--	--	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTCTTATGCAATAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACGTATTTCTTTCACCTTATTACCTTCTTTCT AATACAAGCATATGTTAGAAATTAAGTTCTAGGCATACTT
ESTD- VB12	--	--	--	---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCACCAGACTGAGAACCCACCGTTATATGTACTGGTATCGACAAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	--	---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCTTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTCAATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTCCTGGAGTAGCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCAGTTCGCTGTGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCAGCTCAAGCCTCAGCACCAAGTCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAGCTGTTGGTGGAAAGG AGTGCCCACTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	--	--	--	---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCACTACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCGGGAGTTGGCGAGTAGCGGCTGCAGGCATACACTAAAGTGAAAACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	CCCACTCTATTGGCCAGCCCAAGGACAGAGCTGATCCTTGAACCTTAAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAGGAGGTGCGTCTGCTGCTGCCCGG GTCACTC
EST51976 7	--	--	--	---	---	AGGCAGAACTGGGCCCCCATCGGGGGACGTGGAAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGGTCAACTCCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGACAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGGAGCAGCAGGAGCAGGTGCAGATGCTGGCC CCTTTGGAGAGCTGAGCTGCCCTGGTGC

-301-

EST11458 6	CCACITTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTCATCTTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAAACAATTTCTATGAGCCAGGAGAGATACGATTTCTCGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC	---	---	---	---
EST39852 8	CGGTCTTCTCTCCAGGTATTGTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTCTTGAGGTGAGTACACCTTCCCACTCTCTACGGTACAGAAAGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT	---	---	---	---
EST62448 0	ACCTGGTGTCTGGTGTGGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCTGGGGCCCGTGG TCCTCTGGTGTCTGGGTAGTCTGGAGTCAACGGTCTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGGAACGATGGTCCCCCAGGTGCGGATGGTCAACCCGGACACAAGGGAGAGCGCGGTACCCCTGG CAATAT	---	---	---	---
EST36027 2	AGTGACTTCCAGGAAATGGCTACCCAACTTGCTTCATGCGCCTGTGGCCAACTATGCCTCTCAGA ACATCACTACCACTGCAAGAACAGCAATTGCATACATGATGAGGAGACTGGAAACCTGAAAAAGG CTGCAATCTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGAGGTTCACTTACACT GTTCTTGTAGATGGTCTCTAAAGACAAATGAATGGGGAAGACAA	---	---	---	---
EST12274 0	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTTCCAAATAGAGCCCTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTCAGAACTGTTCTGTCAACCATGGAGGATACATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC	---	---	---	---
EST76807 EST44438 7	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTAGCCGATTGTCTATCTCCAGCGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCCGGCACTGGCTCCGGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCAACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCT GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCCGAGGTGGG	---	---	---	---
EST12839 3	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCCCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTAATCTGAGTAAGGGAACCTGAATGTTATCAACTGG ATTCCAGTAGGTTTCAGTTACTTATGAATATATATGATACCTTAGCTTAG	---	---	---	---
EST54419 8	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCAGCTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTTGGTTTAGCGTGGTGTGATGTTGTCTACTA TAGTCCAAGTGAA	---	---	---	---

EST10398 2	--	--	--	---	---	TGCTGGGTGGCAAGGCTGCAAAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTATCTACTTGATGATGTTTACATTTGGGGCTTGACTTTCCACACGGAGAAG CATTGTTTTCTCGGGCCAAAGGATCTACCAATAGTGTCTATTAGGCATTG
EST36751 7	--	--	--	---	---	CCAAAGTCGTTCAATTTAGCTTTGACAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	--	--	--	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGATCTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCATTATAACAAATATTACCTTTTGAAAAAATAATG AAGGATTTGACCTGCTCGCTCTGGAAGAGTATCCGTCCCTGACGTTTGAACAAATACAGAT GCCTTCCCTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	--	--	--	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCCCTGGCTTCAACACCTACGTCACCTTCCAAAGTAAGGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	---	---	TTCCGCGAGCCCCCATCTCTGGCAACCTGGTCCCCCTCAGGGGCAACCCCGGCACCTCAACGCTCT CGCTCTCGGTAACATCCGCGCGGCGCTCTTGACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGCTCCGCGGCTTGCCAGGGCCAGCCCTGCAGAGAGAGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTTG
EST58707 7	--	--	--	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGCTTT AAGTTCAAGCATCTTTGGCTCACATGAAGGCAAAATCCGAGAGACCTAGAAATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGCTCTGTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGTCTGAAGAACCTT
EST74167 6	--	--	--	---	---	AGACCATGAAGGAGTTGAAGGCTACAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGCGGGCACGGCTGTCCAGGAGCTGCAGGCGCGAGCCCGGCTGGCGGCGGACATGGAGGA CGTGC GGCGCGCTGGTGAGTACCGCGGAGGTGCAGGCCCATGCTGGCCAGAGCACCGAGGAGC TGCGGGTGGCGCTCGCTCCACCTGGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	--	--	--	---	---	CGCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGAGCTGGGGTGGG CCTGGCTCCACCTGCGCAAGCTGGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAAGCGC TGCCAGTGTACAGCGCGCGCGCGGAGGCGCGGAGCGGCTCAGCGGCATCGCGGCATCGCGAGCGCTG GGCGCCCTGGTGAACAGCGCGCGCTGGCGCGCGCACCTGTGGGCTC
EST36770 4	--	--	--	---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGGCTGGGCTGACCAAAATATACTGGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTATACCTCTATTGGAAGGCCCTAAAGAGGCTTATG

EST26021	1	---	---	---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGAGGTTGAGTGACATGTTCCGAACCTGTTCCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACAATTCCTCTGCAGCACTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCAATTATGTGACTGAACCGACTTTTCTAAAGCTCTGAAACAAGAAGCTTTTCTCTTTTGCACAAGACAAAGCAAAGGCC
EST51212	0	---	---	---	---	ATCCTGAGCTCGCCAATAAGCTTCTTGTTCTACTCTCTCTCCACAAGCCCCCAATTTCACTTTCTCAAGAGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTGTGCTCCCACTCAATACAAAAAGGCCCTCTCTACATCT
EST20118	2	---	---	---	---	GTTCGGAATCCTCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGTCGGGCTGTGGTCCAGCTGAGGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGGACGCGGCTCTCTGGGTGCATCCTAAGCTCTGAGAGCAAACTCCCTTGAAGCTGGGAGTGGGTTTAGGGACGCGGGTCTCTGCGTGCATCCTAAGCTCTGAGA
EST53018	6	---	---	---	---	ACAATCCAGTCCACATTCAGAAGAGGAGGGGTGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCAAGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTCTTCCTATGGGATTGACTTTATTTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAGGAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAATAAATTCACAGTCAAGAATCAAGCACTTTTTCGAAACATTGAAGTTGTTTTGAAGTTGGTGTACCTTTAATTACAACCTAGCAGACGGAACTGAACTCAGGGTAAGAAT
EST34088	2	---	---	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAGAGACCGGCTCAAGGATCCCAAGGCCAACTCCCGGAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCTACAGGTAAAG
EST37382	5	---	---	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGGACTTTGAGTCAAAATTGGCTGGACTTGAGTCCCTGAACAGCAAAAGAGAAAAGAGACCCAGAAATCACAGGTGGGCACGTGCGTCTACCGCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082	0	---	---	---	---	TCCAGGGTGGCTGGACCCAGGCCACGCTCTGCAGCAGGAGGACGTGGCTGGCTCGTGAAGCATGTGGGGTGAGCCAGGGGCCAAGGCAGGGCACTGGCTTACGCTCGCTCAGCCCTGCTGTGCACCCAGATCACTGTCTCTGOCATGGCCCTGTGGATGCGCTCTCTGCCCCCTGCTGGCGCTGCTGGCCCTCTGGGACCTGAOCCAGCCGACGCTTTGTGAACCAACACCTGTGGG
EST45311	0	---	---	---	---	GGCCTCCTCTCTCCAAATCTGTCCCTATAGTTTCCCTATTAAAGTGAATACATGCAATCTTTTAGTGGATAGTGCACACAAACACAGAAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAAACACATTTCTGCAAAATCACCTCTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTAGTACATACATCTGTGTCATTGTGTAAT

EST65258 8							TGCCCATCACGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAAACCAGAAAT CCAGTTATTTCCACCTCAAAATGACAGCCATGCCCGCGGTCTTCTGGGGCTCGTCGGGGGG ACAGCTCCACTCTGACTGGCACAGCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3							ATGCAGGATGAAGGTGGACAGGGGAGAGAGGGCCAACTGTCATCCAGGCCCTGCAGATGTCGCTG GACTATGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
							ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCAATTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTCTCCTCGAAGTGCAGTATCCAGAGTTTGGTTTTTGAACGTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTGGGGTTTTTGGTGCATGCA
EST62782 --							GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTGTGCGTTCCACCGATG GAACTGCCGCAATCTGACACGTGTGCACCCAGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCCTGGATGAA
EST68308 5							GGAAGAGATTTAAGAAGCTTGATTTGGACAATCTGTTCTTTGAGTGTGGAAGAGTTTCATGTCTCT GCCTGAGTTACACAGAACTCTTTAGTACAGCGAGTAATAGATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGTTAAGAAAGTAGTATTTTTTA
EST54045 6							GGAATATTAAATATTTTAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTATGATGTGCTATGTGGCAATTTGTTTCTTACAAAATCGGATGGAAATCT GTTAAGTAACTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
EST52908 0							ATCACAGTCTCTGGTCTGCGCCATCATTTCTCTGGGAGAGATGGATGGTGTCTGCAAGCCCTTTGG CAATGTGAGATTGTATG
EST19590 --							AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAATGAC
EST76136 --							TGAAGCTTCTGCCCCAGCTTGCAATGTTTCTAGGAGAACCCGCGTCATACCTTTATCTATAGCCTTCCCC TAGTCTT
EST58607 0							CTCTGGATGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAAGGACAGCCACATGGCGGGATGGCGGGGAGTCTGCTGT TGCGGCCACGGCTGTGGCTCTGTTGTAACGGTAGCCCTTGGGTTGCGATGCCTAAACCTTTGTTTCT TGGCCAAAGGAGGGGGGGTGCCATGCTGAGATGTAGATGCGGCC
							Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.